OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: November 25, 2005, 22:30:27 ; Search time 207 Seconds
(without alignments)
3052.303 Million cell updates/sec

Title: US-10-511-559-73
Perfect score: 7693
Sequence: 1 ATRRYYLGAVELSWDYMQSD..........WWHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7693	100.0	1438	7	ADM75983	Adm75983 Wild-type
2	7693	100.0	1457	2	AAW46246	Aaw46246 Human fac
3	7693	100.0	1457	2	AAW44372	Aaw44372 Human fac
4	7693	100.0	1457	8	ADU47569	Adu47569 Modified
5	7688	99.9	1438	7	ADM75998	Adm75998 Modified
6	7688	99.9	1438	7	ADM75995	Adm75995 Modified
7	7688	99.9	1438	7	ADM75989	Adm75989 Modified
8	7688	99.9	1438	7	ADM75984	Adm75984 Modified
9	7687	99.9	1438	7	ADM75986	Adm75986 Modified
10	7687	99.9	1438	7	ADM75987	Adm75987 Modified
11	7684	99.9	1438	3	AAB01262	Aab01262 B-domain
12	7684	99.9	1438	7	ADF31316	Adf31316 Variant o
13	7684	99.9	1457	7	AAY21675	Aay21675 Beta-doma
14	7684	99.9	1457	7	ADM98124	Adm98124 Human fac
15	7679.5	99.8	1464	8	ADU47624	Adu47624 Human fac
16	7676	99.8	1471	8	ADU47625	Adu47625 Human fac
17	7672	99.7	1479	8	ADU47617	Adu47617 Human fac
18	7668.5	99.7	1440	2	AAR12971	Aar12971 Factor VI
19	7667	99.7	1471	4	AAW23414	Aaw23414 Human B-d
20	7667	99.7	1471	4	AAB67959	Aab67959 Amino aci
21	7666	99.7	1471	8	ADU47608	Adu47608 Human fac
22	7637	99.5	1455	8	ADU47609	Adu47609 Human fac
23	7637	99.3	1461	8	ADU47616	Adu47616 Human fac
24	7635	99.2	1459	4	AAE10832	Aae10832 Human fac
25	7627.5	99.1	1568	8	ADU47621	Adu47621 Human fac
26	7625	99.1	1440	8	ADQ37592	Adq37592 Human fac
27	7625	99.1	1459	4	AAE10833	Aae10833 Human fac
28	7622	99.1	1459	4	AAE10827	Aae10827 Human fac
29	7620.5	99.1	1516	1	AAP80265	Aap80265 Modified
30	7619	99.0	1585	8	ADU47607	Adu47607 Human fac
31	7619	99.0	1585	8	ADU47613	Adu47613 Human fac
32	7614.5	99.0	1447	8	ADQ37595	Adq37595 Human Fac
33	7614	99.0	1428	8	ADQ37589	Adq37589 Human Fac
34	7614	99.0	1440	8	ADQ37607	Adq37607 Human Fac
35	7610	98.9	1453	8	ADU47619	Adu47619 Human fac
36	7604.5	98.8	1450	8	ADU47615	Adu47615 Human fac
37	7603.5	98.8	1437	8	ADQ37593	Adq37593 Human Fac
38	7603	98.8	1447	8	ADQ37610	Adq37610 Human Fac
39	7603	98.8	1428	8	ADQ37604	Adq37604 Human Fac
40	7603	98.8	1444	8	ADQ37596	Adq37596 Human Fac
41	7603	98.8	1457	8	ADU47622	Adu47622 Human fac
42	7601	98.8	1424	4	AAB48842	Aab48842 Mutant ma
43	7601	98.8	1424	8	AAO18622	Aao18622 Human mat
44	7601	98.8	1424	9	ADZ65051	Adz65051 Human mat
45	7599.5	98.8	1441	8	ADQ37597	Adq37597 Human Fac

ALIGNMENTS

RESULT 1
ADM75983
ID   ADM75983 standard; protein; 1438 AA.
XX
AC   ADM75983;
XX
DT   03-JUN-2004 (first entry)
XX
DE   Wild-type B-domain deleted human FVIII protein sequence.
XX
KW   human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
KW   MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
XX
OS   Homo sapiens.
XX
XX
PN   WO2003087161-A1.
XX
PD   23-OCT-2003.
XX
XX
PF   17-APR-2003; 2003WO-EP004063.
XX
PR   18-APR-2002; 2002EP-00008712.
PR   24-MAR-2003; 2003EP-00006554.
XX
PA   (MERE) MERCK PATENT GMBH.
XX
PI   Jones T, Baker M, Carr FJ;
XX
DR   WPI; 2003-845307/78.
XX
PT   New modified human Factor VIII molecule being substantially non-
PT   immunogenic or less immunogenic than non-modified human Factor VIII,
PT   useful in preparing a composition for treating e.g., Gaucher's disease.
XX
PS   Disclosure; Fig 10; 68pp; English.
XX
CC   The invention relates to a novel modified human Factor VIII molecule. The
CC   modified human Factor VIII molecule being substantially non-immunogenic
CC   or less immunogenic than a non-modified human Factor VIII and having
CC   essentially the same biological specificity and activity when used in
CC   vivo. The modified human Factor VIII molecule comprises specifically
CC   altered amino acid residues compared with the non-modified parental
CC   molecule, where the altered amino acid residues cause a reduction or an
CC   elimination of one or more of the T-cell epitopes, which act in the
CC   parental non-modified molecule as MHC class II binding ligands and
CC   stimulate T-cells. The potential MHC class II binding activity peptide is
CC   useful for the manufacture of the modified Factor VIII molecule or a

```
CC   vaccine in order to reduce immunogenicity to Factor VIII in a patient.
CC   The modified Factor VIII molecule is useful in preparing a composition
CC   for treating e.g., Gaucher's disease. This sequence represents a wild-
CC   type B-domain deleted human FVIII protein sequence of the invention.
XX
SQ   Sequence 1438 AA;

Query Match            100.0%;  Score 7693;  DB 7;  Length 1438;
Best Local Similarity  100.0%;  Pred. No.0;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 1438;  Conservative 0;

Qy    1 ATRRYYLGAVELSWDYMQSDLGELPVDARFPPRVPKSFPFNTSVVYKKTLFVEFTDHLFN 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATRRYYLGAVELSWDYMQSDLGELPVDARFPPRVPKSFPFNTSVVYKKTLFVEFTDHLFN 60

Qy   61 IAKPRPPWMGLLGPTIQAEVYDTVVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQ 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 IAKPRPPWMGLLGPTIQAEVYDTVVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQ 120

Qy  121 REKEDDKVFPGGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCR 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 REKEDDKVFPGGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCR 180

Qy  181 EGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDRDAASARAWPKMHTVNGYVNR 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDRDAASARAWPKMHTVNGYVNR 240

Qy  241 SLPGLIGCHRKSVYWHVIGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLL 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 SLPGLIGCHRKSVYWHVIGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLL 300

Qy  301 MDLGQFLLFCHISSHQHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRF 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 MDLGQFLLFCHISSHQHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRF 360

Qy  361 DDDNSPSFIQIRSVAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIG 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 DDDNSPSFIQIRSVAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIG 420

Qy  421 RKYKKVRFMAYTDETFKTREAIQHESGILGPLLYGEVGDTLLIIFKNQASRPYNIYPHGI 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 RKYKKVRFMAYTDETFKTREAIQHESGILGPLLYGEVGDTLLIIFKNQASRPYNIYPHGI 480

Qy  481 TDVRPLYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYYSSFVNME 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TDVRPLYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYYSSFVNME 540

Qy  541 RDLASGLIGPLLICYKESVDORGNQIMSDKRNVILFSVFDENRSWYLTENIQRFLPNPAG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 RDLASGLIGPLLICYKESVDORGNQIMSDKRNVILFSVFDENRSWYLTENIQRFLPNPAG 600

Qy  601 VQLEDPEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKH 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 VQLEDPEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKH 660

Qy  661 KMVYEDTLTLFPFSGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNTGDYYE 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 KMVYEDTLTLFPFSGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNTGDYYE 720

Qy  721 DSYEDISAYLLSKNNAIEPRSFSQNPPVLKRHQREITRTTLQSDQEEIDYDDTISVEMKK 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 DSYEDISAYLLSKNNAIEPRSFSQNPPVLKRHQREITRTTLQSDQEEIDYDDTISVEMKK 780

Qy  781 EDFDIYDEDENQSPRSFQKKTRHYFIAAVERLWDYGMSSSPHVLRNRAQSGSVPQFKKVV 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 EDFDIYDEDENQSPRSFQKKTRHYFIAAVERLWDYGMSSSPHVLRNRAQSGSVPQFKKVV 840

Qy  841 FQEFTDGSFTQPLYRGELNEHLGLLGPYIRAEVEDNIMVTFRNQASRPYSFYSSLISYEE 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 FQEFTDGSFTQPLYRGELNEHLGLLGPYIRAEVEDNIMVTFRNQASRPYSFYSSLISYEE 900

Qy  901 DQRQGAEPRKNFVKPNETKTYFWKVQHHMAPTKDEFDCKAWAYFSDVDLEKDVHSGLIGP 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 DQRQGAEPRKNFVKPNETKTYFWKVQHHMAPTKDEFDCKAWAYFSDVDLEKDVHSGLIGP 960

Qy  961 LLVCHTNTLNPAHGRQVTVQEFALFFTIFDETKSWYFTENMERNCRAPCNIQMEDPTFKE 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 LLVCHTNTLNPAHGRQVTVQEFALFFTIFDETKSWYFTENMERNCRAPCNIQMEDPTFKE 1020

Qy 1021 NYRFHAINGYIMDTLPGLVMAQDQRIRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMA 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 NYRFHAINGYIMDTLPGLVMAQDQRIRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMA 1080

Qy 1081 LYNLYPGVFETVEMLPSKAGIWRVECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRD 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 LYNLYPGVFETVEMLPSKAGIWRVECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRD 1140

Qy 1141 FQITASGQYGQWAPKLARLHYSGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFS 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 FQITASGQYGQWAPKLARLHYSGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFS 1200

Qy 1201 SLYISQFIIMYSLDGKKWQTYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPT 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 SLYISQFIIMYSLDGKKWQTYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPT 1260

Qy 1261 HYSIRSTLRMELMGCDLNSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQG 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 HYSIRSTLRMELMGCDLNSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQG 1320

Qy 1321 RSNAWRPQVNNPKEWLQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLF 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 RSNAWRPQVNNPKEWLQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLF 1380

Qy 1381 FQNGKVKVFQGNQDSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY 1438
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 FQNGKVKVFQGNQDSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY 1438
```

RESULT 2

AAW46246
```
ID   AAW46246 standard; protein; 1457 AA.
XX
AC   AAW46246;
XX
DT   25-MAR-2003 (revised)
DT   06-AUG-1998 (first entry)
XX
DE   Human factor VIII beta-domain deleted SQN deletion protein sequence.
XX
KW   Replication defective; recombinant retrovirus; RRV; therapeutic protein;
KW   haemophilia; thrombosis; hypercoagulable disorder; liver disease; human;
KW   hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; diabetes;
KW   cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemi;
KW   hypopituitarism; adenine deaminase deficiency; HIV infection; anaemia;
KW   Gaucher's syndrome; high blood pressure; Alzheimer's disease, autoimmune;
KW   inflammatory disease; factor VIII.
XX
OS   Homo sapiens.
XX
PN   WO9800541-A2.
XX
PD   08-JAN-1998.
XX
PF   02-JUL-1997; 97WO-US011784.
XX
PR   02-JUL-1996; 96US-00645601.
PR   13-AUG-1996; 96US-00696381.
PR   04-JUN-1997; 97US-00869309.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Jolly DJ, Barber JR, Chang SMW, Respess JG, Allen JR, Boder M;
PI   Chong K, De La Vega D, Depolo NJ, Hsu DC, Ibanez CE;
PI   Mittelstaedt DM, Prussak CE, Greengard J, Lee R;
XX
DR   WPI; 1998-086966/08.
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OM protein - protein search, using sw model

Run on: November 25, 2005, 22:33:30 ; Search time 53 Seconds
(without alignments)
2610.560 Million cell updates/sec

Title: US-10-511-559-73
Perfect Score: 7693
Sequence: 1 ATRRYLGAVELSWDYMQSD..........WVHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   PIR_80:*
          1: pir1:*
          2: pir2:*
          3: pir3:*
          4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7236	94.1	2351	1	EZHU	coagulation factor
2	6236	81.1	2133	2	T42763	coagulation factor
3	6201	80.6	2319	2	A47004	coagulation factor
4	2391.5	31.1	2224	2	KFHU5	coagulation factor
5	2371	30.8	2183	2	T42764	coagulation factor
6	2370	30.8	2211	2	KFBO5	coagulation factor
7	1740.5	22.6	1069	2	KUHU	coagulation factor
8	1696.5	22.1	1059	1	A35210	ferroxidase (EC 1.
9	1104	14.4	216	2	A44258	ferroxidase
10	663	8.6	427	2	JC4915	factor VIII-associ
11	657	8.5	463	2	A36479	ags protein precur
12	650	8.4	409	2	T11743	milk fat globule m
13	635	8.3	401	2	S65138	pp47 protein - pig
14	635	8.3	427	2	S74211	glycoprotein antig
15	543	7.1	869	2	A25945	PAS-6/7 protein pr
16	443	5.8	927	1	JQ0948	coagulation factor
17	424.5	5.5	218	2	A47285	A5 antigen precurs
18	306.5	4.0	3133	2	S52093	hemocytin - silkwo
19	262	3.4	845	2	JC5256	adipocyte transcri
20	221	2.9	719	2	S51739	transcription repr
21	211	2.7	1283	2	T13799	neurexin IV - frui
22	207.5	2.7	737	2	T31349	hypothetical prote
23	206.5	2.7	737	2	T15615	hypothetical prote
24	192	2.5	913	2	A48280	receptor tyrosine
25	192	2.5	876	2	A49508	protein-tyrosine k
26	185.5	2.4	855	2	S42621	protein-tyrosine k
27	185.5	2.4	910	2	S43137	tyrosine kinase re
28	173.5	2.3	819	2	I48859	tyro 10 receptor k
29	171	2.2	1381	2	T31083	paranodin - rat
30	149.5	2.2	1385	2	T14158	neurexin IV - mous
31	149	1.9	578	2	S66353	L-ascorbate oxidas
32	148	1.9	1883	2	G82875	hypothetical prote
33	148	1.9	622	2	S62580	probable multicopp
34	141.5	1.9	1196	2	S46430	botulinum neurotox
35	140.5	1.8	1196	2	JQ1467	toxin, nontoxic co
36	140.5	1.8	1217	2	T18209	mxnG protein - Bac
37	139	1.8	1193	2	JC4901	nontoxic-nonhemagg
38	137.5	1.8	580	2	F84828	probable laccase (
39	137.5	1.8	903	2	F82080	preprotein translo
40	136.5	1.8	2657	2	T18497	hypothetical prote
41	135	1.8	343	2	T35030	probable copper ox
42	135	1.8	791	2	T16031	hypothetical prote
43	134.5	1.7	1132	2	H82887	hypothetical prote
44	133.5	1.7	567	2	T44928	L-ascorbate oxidas
45	133.5	1.7	2925	2	T00133	RNA-directed RNA p

ALIGNMENTS

RESULT 1
EZHU
coagulation factor VIII precursor [validated] - human
N;Alternate names: antihemophilic factor A; coagulation factor VIIIc; procoagulant compor
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 31-Dec-2004
C;Accession: I54318; A00525; I58059; A23584; A26174; A42348; A43986; S63527; S66445; B42
R;Gitschier, J.; Wood, W.I.
A;Molecule type: DNA
A;Residues: 1-1921; S',1923-2351 <RES>
A;Cross-references: UNIPROT:P00451; UNIPARC:UPI000016ABD3; GB:M88648; NID:g182381; PIDN:/
A;Accession: I54318
A;Status: preliminary; translated from GB/EMBL/DDBJ
Hum. Mol. Genet. 1, 199-200, 1992
A;Title: Sequence of the exon-containing regions of the human factor VIII gene.
A;Reference number: I54318; MUID:93265012; PMID:1303178
A;Accession: I54318
A;Status: preliminary; translated from GB/EMBL/DDBJ
Nature 312, 330-337, 1984
A;Title: Expression of active human factor VIII from recombinant DNA clones.
A;Reference number: A00525; MUID:85061548; PMID:6438526
R;Wood, W.I.; Capon, D.J.; Simonsen, C.C.; Eaton, D.L.; Gitschier, J.; Keyt, B.; Seeburg,
Nature 312, 330-337, 1984
A;Accession: A00525
A;Molecule type: mRNA
A;Residues: 1-2351 <WOO>
R;Toole, J.J.; Knopf, J.L.; Wozney, J.M.; Sultzman, L.A.; Buecker, J.L.; Pittman, D.D.; F
s, D.N.; Hewick, R.M.
Nature 312, 342-347, 1984
A;Title: Molecular cloning of a cDNA encoding human antihaemophilic factor.
C;Date: 28-Aug-1985
C;Accession: I54318; A00525; I58059; A23584; A26174; A42348; A43986; S63527; B42
A;Reference number: I58059; MUID:85061550; PMID:6438528
A;Accession: I58059
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-74,'V',76-1259,'E',1261-2351 <RE2>
A;Cross-references: UNIPARC:UPI0000144860; GB:K01740; NID:g182802; PIDN:AAA52484.1; PID:g
R;Truett, M.A.; Blacher, R.; Burke, R.L.; Caput, D.; Chu, C.; Dina, D.; Hartog, K.; Kuo,
.B.; Randolph, A.; Urdea, M.S.; Valenzuela, P.; Dahl, H.H.; Favaloro, J.; Hansen, J.; Not
DNA 4, 333-349, 1985
A;Title: Characterization of the polypeptide composition of human factor VIII:C and the r
A;Reference number: A23584; MUID:86081164; PMID:3935400
A;Accession: A23584
A;Molecule type: mRNA
A;Residues: 1-2351 <TRU>
R;Eaton, D.; Rodriguez, H.; Vehar, G.A.
Biochemistry 25, 505-512, 1986
A;Title: Proteolytic processing of human factor VIII. Correlation of specific cleavages k
ity.
A;Reference number: A26174; MUID:86159740; PMID:3082357
A;Accession: A26174
A;Molecule type: protein
A;Residues: 20-36,392-399,'X',401-402,1668-1678,1709-1722,'D',1723-1725,1741-1755 <EAT>
A;Cross-references: UNIPARC:UPI000017229C; UNIPARC:UPI000017229D;

R;Pittman, D.D.; Wang, J.H.; Kaufman, R.J.
Biochemistry 31, 3315-3325, 1992
A;Title:Identification and functional importance of tyrosine sulfate residues within re
A;Reference number: A42348; MUID:92207952; PMID:1554716
A;Accession: A42348
A;Molecule type: protein
A;Residues: 20-36;356-371,392-408,582-594;1668-1669,'X',1671,1672-1692,1693-1708,1709-17
A;Cross-references: UNIPARC:UPI000172296; UNIPARC:UPI000017229B; UNIPARC:UPI000017229C;
2A1
A;Experimental source: recombinant material from Chinese hamster ovary cells
A;Note: sequence extracted from NCBI backbone and corrected to correspond with the publi
R;Fay, P.J.; Smudzin, T.M.
J. Biol. Chem. 264, 14005-14010, 1989
A;Title: Intersubunit fluorescence energy transfer in human factor VIII.
A;Reference number: A43986; MUID:89340500; PMID:2503509
A;Accession: A43986
A;Molecule type: protein
A;Residues: 'X',517-523;1853-1860,'X',1862-1864,'X',1866 <FAY>
A;Cross-references: UNIPARC:UPI00017229A2; UNIPARC:UPI00017229A3
R;Leyte, A.; van Schijndel, H.B.; Niehrs, C.; Huttner, W.B.; Verbeet, M.P.; Mertens, K.;
J. Biol. Chem. 266, 740-746, 1991
A;Title: Sulfation of Tyr(1680) of human blood coagulation factor VIII is essential for
A;Reference number: A56109; MUID:91093266; PMID:1898735
A;Contents: annotation; sulfation
R;Gitschier, J.; Wood, W.I.; Goralka, T.M.; Wion, K.L.; Chen, E.Y.; Eaton, D.H.; Vehar,
Nature 312, 326-330, 1984
A;Title: Characterization of the human factor VIII gene.
A;Reference number: A56196; MUID:85061547; PMID:6438525
A;Contents: annotation; introns
R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.; Hedner, U.; Ezban, M.
Protein Sci. 4, 740-746, 1995
A;Title: Locations of disulfide bonds and free cysteines in the heavy and light chains o
A;Reference number: A56216; MUID:95538127; PMID:7613471
A;Contents: annotation; disulfide bonds
A;Note: 329-Cys, 711-Cys, and 2019-Cys were shown to have free sulfhydryls
R;Kjalke, M.; Heding, A.; Talbo, G.; Persson, E.; Thomsen, J.; Ezban, M.
Eur. J. Biochem. 234, 773-779, 1995
A;Title: Amino acid residues 721-729 are required for full factor VIII activity.
A;Reference number: S63527; MUID:96163459; PMID:8575434
A;Accession: S63527
A;Molecule type: protein
A;Status: Preliminary
A;Residues: 733-752;753-759 <KJA>
R;Lind, P.; Larsson, K.; Spira, J.; Sydow-Baeckman, M.; Almstedt, A.; Gray, E.; Sandberg
Eur. J. Biochem. 232, 19-27, 1995
A;Title: Novel forms of B-domain-deleted recombinant factor VIII molecules. Construction
A;Reference number: S66445; MUID:96048024; PMID:7556150
A;Accession: S66445
A;Molecule type: protein
A;Residues: 1668-1685 <LIN>
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A;Comment: Factor VIII is activated by factor Xa and thrombin, but prolonged exposure pr
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C;Gene: GDB:F8C
A;Map position: Xq28-Xq28
C;Cross-references: GDB:119124; OMIM:306700
C;Introns: 48/2; 89/1; 130/1; 201/1; 224/1; 263/1; 337/1; 424/2; 481/3; 513/1; 584/3; 63
C;Function:
A;Description: acts as a cofactor, with calcium and phospholipid, for the factor IXa pro
A;Pathway: blood coagulation
C;Superfamily: coagulation factors V/VIII; discoidin I amino-terminal homology; ferroxid
C;Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A; pla
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F;20-740/Product: coagulation factor VIII heavy chain #status experimental <ACH>
F;20-2351/Product: coagulation factor VIII #status experimental <MAT>
F;20-356/Domain: A1 <DA1>
F;23-348/Domain: ferroxidase repeat homology <FO1>
F;392-759/Domain: A2 <DA2>
F;402-759/Domain: ferroxidase repeat homology <FO2>
F;760-1667/Domain: B <DB>
F;1668-2351/Product: coagulation factor VIII light chain #status experimental <ACL>
F;1709-2038/Domain: A3 <DA3>
F;1716-2038/Domain: ferroxidase repeat homology <FO3>
F;2039-2191/Domain: C1 <DC1>
F;2039-2188/Domain: discoidin I amino-terminal homology <DN1>
F;2192-2351/Domain: C2 <DC2>
F;2192-2345/Domain: discoidin I amino-terminal homology <DN2>
F;60,258,601,776,803,847,919,962,982,1020,1024,1074,1085,1204,1274,1278,1301,1319,1403,1
F;172-198,267-348,547-573,649-730,1851-1877,1918-1922,2040-2188/Disulfide bonds: #status
F;355-356/Cleavage site: Arg-Met (coagulation factor Xa, protein C) #status predicted
F;365,737,738,742,1683,1699/Binding site: sulfate (Tyr) (covalent) #status experimental
F;391-392/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimental
F;414,426/Binding site: sulfate (Tyr) (covalent) #status experimental
F;759-760/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status predicted
F;1667-1668/Cleavage site: Arg-Glu (unidentified proteinase) #status experimental
F;1708-1709/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimenta
F;1740-1741/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experiment
F;2193-2345/Disulfide bonds: #status predicted

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Best Local Similarity   61.%;   Pred. No. 0;
Matches 1438;   Conservative   0;   Mismatches   0;   Indels   894;   Gaps   1;

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Qy  121 REKEDDKVFPGGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCR  180
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Qy  241 SLPGLIGCHRKSVYWHVIGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLL  300
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Qy  301 MDLGQFLLFCHISSHQHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRF  360
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Qy  421 RKYKKVRFMAYTDETFKTREAIQHESGILGPLLYGEVGDTLLIIFKNQASRPYNIYPHGI  480
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Qy  481 TDVRPLYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYYSSFVNME  540
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Db  500 TDVRPLYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYYSSFVNME  559

Qy  541 RDLASGLIGPLLICYKESVDQRGNQIMSDKRNVILFSVFDENRSWYLTENIQRFLPNPAG  600
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Db  560 RDLASGLIGPLLICYKESVDQRGNQIMSDKRNVILFSVFDENRSWYLTENIQRFLPNPAG  619

Qy  601 VQLEDPEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKH  660
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Qy  661 KMVYEDTLTLFPFSGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNTGDYYE  720
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Qy  721 DSYEDISAYLLSKNNAIEPRSF-------------------------------------  742
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Db  740 DSYEDISAYLLSKNNAIEPRSFSQNSRHPSTRQKQFNATTIPENDIEKTDPWFAHRTPMP  799
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 25, 2005, 22:32:09 ; Search time 270 Seconds
(without alignments)
3757.591 Million cell updates/sec

Title: US-10-511-559-73
Perfect Score: 7693
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Accession	Description
1	7236	94.1	2351	1	FA8_HUMAN	P00451	h coagulati
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3	6281	81.6	2343	1	FA8_CANFA	O18806	canis famil
4	6236	81.1	2133	1	FA8_PIG	P12263	sus scrofa
5	6201	80.6	2319	1	FA8_MOUSE	Q06194	mus musculu
6	4967.5	64.6	2258	2	Q7TN96_RAT	Q7tn96	rattus norv
7	3236	42.1	1639	2	Q804W6_FUGRU	Q804w6	fugu rubrip
8	2672.5	34.5	1459	2	Q593B6_PSETE	Q593b6	pseudonaja
9	2652	34.5	1460	2	Q7SZN0_PSETE	Q7szn0	pseudonaja
10	2650.5	34.5	1459	2	Q58L91_9SAUR	Q58l91	oxyuranus s
11	2631	34.2	1460	2	Q58I90_OXYMI	Q58i90	oxyuranus m
12	2542	33.0	1802	2	Q804W5_FUGRU	Q804w5	fugu rubrip
13	2490.5	32.4	2119	2	Q90X47_BRARE	Q90x47	brachydanio
14	2394.5	31.1	2224	1	FA5_HUMAN	P12259	homo sapien
15	2387	31.0	2224	2	Q5R347_HUMAN	Q5r347	homo sapien
16	2380	30.9	1304	2	Q4RPE7_TETNG	Q4rpe7	tetraodon n
17	2375	30.9	2229	2	Q5R346_HUMAN	Q5r346	homo sapien
18	2371	30.8	2183	2	O88783_MOUSE	O88783	mus musculu
19	2370	30.8	2211	1	FA5_BOVIN	O28107	bos taurus
20	2355.5	30.6	2258	1	FA5_PIG	Q9igp1	sus scrofa
21	2326.5	30.2	1377	2	Q804X3_CHICK	Q804x3	gallus gall
22	2326	30.2	1725	2	Q4S9Q1_TETNG	Q4s9q1	tetraodon n
23	2093	27.2	1157	1	HEPH_MOUSE	Q920h8	mus musculu
24	1809	23.3	1157	1	HEPH_RAT	Q9z0h8	rattus norv
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26	1751	22.8	1158	2	Q5JUU0_HUMAN	Q5juu0	homo sapien
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30	1736.5	22.6	1065	1	Q9JL97_RAT	Q9jl97	rattus norv
31	1718.5	22.3	1084	2	Q4TBZ9_TETNG	Q4tbz9	tetraodon n
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34	1644.5	21.4	1062	1	CERU_MOUSE	Q61147	mus musculu
35	1627	21.1	1048	2	Q9XT27_SHEEP	Q9xt27	ovis aries
36	1601.5	20.8	349	2	Q684Q7_MOUSE	Q684q7	mus musculu
37	1599.5	20.8	2102	2	Q7TPK2_RAT	Q7tpk2	rattus norv
38	1589.5	20.7	1007	2	Q4SFU7_TETNG	Q4sfu7	tetraodon n
39	1543.5	20.1	745	2	Q8BQ43_MOUSE	Q8bq43	mus musculu
40	1443.5	18.8	355	2	Q804X4_CHICK	Q804x4	gallus gall
41	1341	17.4	891	2	Q5JUU1_HUMAN	Q5juu1	homo sapien
42	1183.5	15.4	811	2	Q5JZ08_HUMAN	Q5jz08	homo sapien
43	1104	14.4	216	2	O14286_HUMAN	O14286	homo sapien
44	1078	14.0	248	2	Q5RAM1_PONPY	Q5ram1	pongo pygma
45	1046.5	13.6	626	2	Q90ZT2_BRARE	Q90zt2	brachydanio

ALIGNMENTS

RESULT 1
FA8_HUMAN

```
ID   FA8_HUMAN     STANDARD;     PRT;   2351 AA.
AC   P00451;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Coagulation factor VIII precursor (procoagulant component)
DE   (Antihemophilic factor) (AHF) (Contains: Factor VIIIa heavy chain, 200
DE   kDa isoform; Factor VIIIa heavy chain, 92 kDa isoform; Factor VIII B
DE   chain; Factor VIIIa light chain).
GN   Name=F8; Synonyms=F8C;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86081164; PubMed=3935400;
RA   Truett M.A., Blacher R., Burke R.L., Caput D., Chu C., Dina D.,
RA   Hartog K., Kuo C.H., Masiarz F.R., Merryweather J.P., Najarian R.,
RA   Pachl C., Potter S.J., Puma J., Quiroga M., Rall L.B., Randolph A.,
RA   Urdea M.S., Valenzuela P., Dahl H.-H.M., Favalaro J., Hansen J.,
RA   Nordfang O., Ezban M.;
RT   "Characterization of the polypeptide composition of human factor
RT   VIII:C and the nucleotide sequence and expression of the human kidney
RT   cDNA.";
RL   DNA 4:333-349(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=85061548; PubMed=6438526;
RA   Wood W.I., Capon D.J., Simonsen C.C., Eaton D.L., Gitschier J.,
RA   Keyt B., Seeburg P.H., Smith D.H., Hollingshead P., Wion K.L.,
RA   Delwart E., Tuddenham E.G.D., Vehar G.A., Lawn R.M.;
RT   "Expression of active human factor VIII from recombinant DNA clones.";
RL   Nature 312:330-337(1984).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=85061550; PubMed=6438528;
RA   Toole J.J., Knopf J.L., Wozney J.M., Sultzman L.A., Buecker J.L.,
RA   Pittman D.D., Kaufman R.J., Brown E., Shoemaker C., Orr E.C.,
RA   Amphlett G.W., Foster W.B., Coe M.L., Knutson G.J., Fass D.N.,
RA   Hewick R.M.;
RT   "Molecular cloning of a cDNA encoding human antihaemophilic factor.";
RL   Nature 312:342-347(1984).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=93265012; PubMed=1303178;
RA   Gitschier J., Wood W.I.;
RT   "Sequence of the exon-containing regions of the human factor VIII
RT   gene.";
RL   Hum. Mol. Genet. 1:199-200(1992).
RN   [5]
```

RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLU-1260 AND VAL-2257.
RA   Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA   Rajkumar N., Yi Q., Nickerson D.A.;
RT   "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 2064-2070.
RA   de Water N.S., Williams R., Browett P.J.;
RT   "Factor VIII gene normal intron 20 sequence.";
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SULFATION OF TYR-1699.
RA   Leyte A., van Schijndel H.B., Niehrs C., Huttner W.B., Verbeet M.P.,
RA   Mertens K., van Mourik J.A.;
RT   "Sulfation of Tyr1680 of human blood coagulation factor VIII is
RT   essential for the interaction of factor VIII with von Willebrand
RT   factor.";
RL   J. Biol. Chem. 266:740-746(1991).
RN   [8]
RP   SULFATION.
RX   MEDLINE=92207952; PubMed=1554716;
RA   Pittman D.D., Wang J.H., Kaufman R.J.;
RT   "Identification and functional importance of tyrosine sulfate residues
RT   within recombinant factor VIII.";
RL   Biochemistry 31:3315-3325(1992).
RN   [9]
RP   SULFATION SITES TYR-737; TYR-738 AND TYR 742, AND DISULFIDE BONDS.
RX   MEDLINE=95338127; PubMed=7613471;
RA   McMullen B.A., Fujikawa K., Davie E.W., Hedner U., Ezban M.;
RT   "Locations of disulfide bonds and free cysteines in the heavy and
RT   light chains of recombinant human factor VIII (antihemophilic factor
RT   A).";
RL   Protein Sci. 4:740-746(1995).
RN   [10]
RP   STRUCTURE BY NMR OF 2322-2343.
RX   MEDLINE=95200924; PubMed=7893714;
RA   Gilbert G.E., Baleja J.D.;
RT   "Membrane-binding peptide derived from the C2 domain of factor VIII forms an
RT   amphipathic structure as determined by NMR spectroscopy.";
RL   Biochemistry 34:3022-3031(1995).
RN   [11]
RP   REVIEW ON MOLECULAR BASIS OF HEMA.
RX   MEDLINE=91221499; PubMed=1902642;
RA   Gitschier J.;
RT   "The molecular basis of hemophilia A.";
RL   Ann. N. Y. Acad. Sci. 614:89-96(1991).
RN   [12]
RP   REVIEW ON MOLECULAR BASIS OF HEMA.
RX   MEDLINE=89088506; PubMed=2491949;
RA   White G.C. II, Shoemaker C.B.;
RT   "Factor VIII gene and hemophilia A.";
RL   Blood 73:1-12(1989).
RN   [13]
RP   REVIEW ON MOLECULAR BASIS OF HEMA.
RX   MEDLINE=95245332; PubMed=7728145;
RA   Antonarakis S.E., Kazazian H.H. Jr., Tuddenham E.G.D.;
RT   "Molecular etiology of factor VIII deficiency in hemophilia A.";
RL   Hum. Mutat. 5:1-22(1995).
RN   [14]
RP   VARIANT HEMA GLN-2326.
RX   MEDLINE=86235434; PubMed=3012775;
RA   Gitschier J., Wood W.I., Shuman M.A., Lawn R.M.;
RT   "Identification of a missense mutation in the factor VIII gene of a
RT   mild hemophiliac.";
RL   Science 232:1415-1416(1986).
RN   [15]
RP   VARIANT HEMA PRO-2135.
RX   MEDLINE=88096539; PubMed=3122181;
RA   Levinson B., Janco R.L., Phillips J.A. III, Gitschier J.;
RT   "A novel missense mutation in the factor VIII gene identified by
RT   analysis of amplified hemophilia DNA sequences.";

RL   Nucleic Acids Res. 15:9797-9805(1987).
RN   [16]
RP   VARIANT HEMA GLN-2228.
RX   MEDLINE=88191889; PubMed=2833855;
RA   Youssoufian H., Antonarakis S.E., Bell W., Griffin A.M.,
RA   Kazazian H.H. Jr.;
RT   "Nonsense and missense mutations in hemophilia A:
RT   relative mutation rate at CG dinucleotides.";
RL   Am. J. Hum. Genet. 42:718-725(1988).
RN   [17]
RP   VARIANT HEMA GLY-291.
RX   MEDLINE=88220354; PubMed=2835904;
RA   Youssoufian H., Wong C., Aronis S., Platokoukis H., Kazazian H.H. Jr.,
RA   Antonarakis S.E.;
RT   "Moderately severe hemophilia A resulting from Glu-->Gly substitution
RT   in exon 7 of the factor VIII gene.";
RL   Am. J. Hum. Genet. 42:867-871(1988).
RN   [18]
RP   VARIANT HEMA CYS-1708.
RX   MEDLINE=89274393; PubMed=2499363;
RA   O'Brien D.P., Tuddenham E.G.;
RT   "Purification and characterization of factor VIII 1,689-Cys: a
RT   nonfunctional cofactor occurring in a patient with severe hemophilia
RT   A.";
RL   Blood 73:2117-2122(1989).
RN   [19]
RP   VARIANT HEMA CYS-391.
RX   MEDLINE=90001543; PubMed=2506948;
RA   Shima M., Ware J., Yoshioka A., Fukui H., Fulcher C.A.;
RT   "An arginine to cysteine amino acid substitution at a critical
RT   thrombin cleavage site in a dysfunctional factor VIII molecule.";
RL   Blood 74:1612-1617(1989).
RN   [20]
RP   VARIANT HEMA LEU-189.
RX   MEDLINE=90057680; PubMed=2510835;
RA   Chan V., Chan T.K., Tong T.M., Todd D.;
RT   "A novel missense mutation in exon 4 of the factor VIII:C gene
RT   resulting in moderately severe hemophilia A.";
RL   Blood 74:2688-2691(1989).
RN   [21]
RP   VARIANT HEMA CYS-2326.
RX   MEDLINE=89197216; PubMed=2495245;
RA   Inaba H., Fujimaki M., Kazazian H.H. Jr., Antonarakis S.E.;
RT   "Mild hemophilia A resulting from Arg-to-Leu substitution in exon 26
RT   of the factor VIII gene.";
RL   Hum. Genet. 81:335-338(1989).
RN   [22]
RP   VARIANT HEMA HIS-391.
RX   MEDLINE=89264602; PubMed=2498882;
RA   Arai M., Inaba H., Higuchi M., Antonarakis S.E., Kazazian H.H. Jr.,
RA   Fujimaki M., Hoyer L.W.;
RT   "Direct characterization of factor VIII in plasma; detection of a
RT   mutation altering a thrombin cleavage site (arginine-
RT   372--histidine).";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:4277-4281(1989).
RN   [23]
RP   VARIANT HEMA CYS-1708.
RX   MEDLINE=90105723; PubMed=2104766;
RA   Arai M., Higuchi M., Antonarakis S.E., Kazazian H.H. Jr.,
RA   Phillips J.A. III, Janco R.L., Hoyer L.W.;
RT   "Characterization of a thrombin cleavage site mutation (Arg 1689 to
RT   Cys) in the factor VIII gene of two unrelated patients with cross-
RT   reacting material-positive hemophilia A.";
RL   Blood 75:384-389(1990).
RN   [24]
RP   VARIANTS HEMA GLN-2228 AND LEU-2326.
RX   MEDLINE=90123183; PubMed=2105106;
RA   Casula L., Murru S., Pecorara M., Ristaldi M.S., Restagno G.,
RA   Mancuso G., Morfini M., de Biasi R., Baudo F., Carbonara A.;
RT   "Recurrent mutations and three novel rearrangements in the factor VIII
RT   gene of hemophilia A patients of Italian descent.";
RL   Blood 75:662-670(1990).
RN   [25]

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2005, 22:42:11 ; Search time 52 Seconds
(without alignments)
2286.301 Million cell updates/sec

Title: US-10-511-559-73
Perfect score: 7693
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7693	100.0	1457	2	US-09-001-039B-47	Sequence 47, Appl
2	7684	99.9	1438	2	US-09-209-916-1	Sequence 1, Appli
3	7667	99.7	1471	1	US-08-683-839B-3	Sequence 3, Appli
4	7597	98.8	1447	2	US-09-407-605-4	Sequence 4, Appli
5	7587	98.6	1445	2	US-09-407-605-3	Sequence 3, Appli
6	7443	96.8	1661	1	US-08-882-083-2	Sequence 2, Appli
7	7443	96.8	1661	1	US-08-558-107-2	Sequence 2, Appli
8	7443	96.8	1661	2	US-09-243-539-2	Sequence 2, Appli
9	7236	94.1	2332	2	US-10-360-101-229	Sequence 229, App
10	7236	94.1	2351	1	US-08-366-851A-2	Sequence 2, Appli
11	7236	94.1	2351	2	US-10-133-907-4	Sequence 4, Appli
12	7236	94.1	2351	2	US-09-001-039B-45	Sequence 45, Appl
13	7233	94.0	2332	2	US-08-276-594A-2	Patent No. 5171844
14	7230	94.0	2351	6	US-07-864-004B-4	Sequence 4, Appli
15	7227	93.9	2332	1	US-08-251-937A-4	Sequence 4, Appli
16	7227	93.9	2332	1	US-08-212-133A-2	Sequence 2, Appli
17	7227	93.9	2332	1	US-08-474-503-2	Sequence 2, Appli
18	7227	93.9	2332	1	US-08-670-707A-2	Sequence 2, Appli
19	7227	93.9	2332	1	US-09-037-601-2	Sequence 2, Appli
20	7227	93.9	2332	2	US-09-315-179-2	Sequence 2, Appli
21	7227	93.9	2332	2	US-09-523-656-2	Sequence 2, Appli
22	7227	93.9	2332	2	US-09-957-641A-2	Sequence 2, Appli
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26	7227	93.9	2351	1	US-08-121-202-2	Sequence 2, Appli
27	7218	93.8	2351	6	S422260-1	Patent No. 5422260
28	7188	93.4	2332	2	US-09-324-867-3	Sequence 3, Appli
29	6569	85.4	1467	2	US-09-523-656-38	Sequence 38, Appl
30	6498	84.5	1443	1	US-08-670-707A-39	Sequence 39, Appl
31	6498	84.5	1443	2	US-09-037-601-39	Sequence 39, Appl
32	6498	84.5	1443	2	US-09-315-179-39	Sequence 39, Appl
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34	6236	81.1	2133	1	US-08-670-707A-37	Sequence 37, Appl
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37	6201	80.6	2133	1	US-08-212-133A-8	Sequence 8, Appli
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us-10-511-559-73.rai

ALIGNMENTS

RESULT 1
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Sequence 47, Application US/0901039B
; Patent No. 6818439
GENERAL INFORMATION:
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Respess, James G.
; APPLICANT: DePolo, Nicholas J.
; APPLICANT: Hsu, David Chi-Tang
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Greengard, Judith
; APPLICANT: Lee, Will
; TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF
; TITLE OF INVENTION: RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT
; TITLE OF INVENTION: OF HEMOPHILIA AND OTHER DISORDERS
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,039B
; FILING DATE: 13-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-001-039B-47

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Qy   181 EGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDRDAASARAWPKMHTVNGYVNR  240
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Qy   301 MDLGQFLLFCHISSHQHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRF  360
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Qy  1141 FQITASGQYGQWAPKLARLHYSGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFS 1200
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Qy  1201 SLYISQFIIMYSLDGKKWQTYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPT 1260
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 25, 2005, 22:42:31 ; Search time 193 seconds.

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Perfect score: 7693
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	7684	99.9	1438	4	US-10-047-257-1	Sequence 1, Appli
3	7684	99.9	1438	4	US-10-225-900-1	Sequence 1, Appli
4	7667	99.7	1457	5	US-10-813-507-13	Sequence 13, Appli
5	7667	99.7	1471	4	US-10-095-718-2	Sequence 2, Appli
6	7667	99.7	1471	4	US-10-681-970-2	Sequence 2, Appli
7	7635	99.2	1459	4	US-10-239-498A-13	Sequence 13, Appli
8	7625	99.1	1459	4	US-10-239-498A-15	Sequence 15, Appli
9	7622	99.1	1459	4	US-10-239-498A-4	Sequence 4, Appli
10	7601	98.8	1424	5	US-10-472-516-5	Sequence 5, Appli
11	7601	98.8	1424	5	US-10-968-286-5	Sequence 5, Appli
12	7282	94.7	1457	5	US-10-813-507-17	Sequence 17, Appli
13	7236	94.1	2332	4	US-10-360-101-229	Sequence 229, App
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15	7236	94.1	2332	4	US-10-721-997A-34	Sequence 34, Appli
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18	7236	94.1	2351	4	US-10-172-712-27	Sequence 27, Appli
19	7236	94.1	2351	4	US-10-133-907-4	Sequence 4, Appli
20	7236	94.1	2351	4	US-10-411-037-30	Sequence 30, Appli
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22	7236	94.1	2351	4	US-10-410-026-30	Sequence 30, Appli
23	7236	94.1	2351	4	US-10-411-049-30	Sequence 30, Appli
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28	7236	94.1	2351	4	US-10-410-913-30	Sequence 30, Appl
29	7236	94.1	2351	5	US-10-789-956-1	Sequence 1, Appli
30	7236	94.1	2351	5	US-10-472-516-2	Sequence 2, Appli
31	7236	94.1	2351	5	US-10-410-980-30	Sequence 30, Appli
32	7236	94.1	2351	5	US-10-410-897-30	Sequence 30, Appl
33	7236	94.1	2351	5	US-10-968-286-2	Sequence 2, Appli
34	7236	94.1	2351	3	US-10-492-261-30	Sequence 30, Appl
35	7236	93.9	2332	4	US-09-957-641-2	Sequence 2, Appli
36	7227	93.9	2332	4	US-10-187-319-2	Sequence 2, Appli
37	7227	93.9	2332	4	US-10-131-510A-2	Sequence 2, Appli
38	7227	93.9	2332	4	US-10-445-235-2	Sequence 2, Appli
39	7227	93.9	2332	4	US-10-239-498A-2	Sequence 2, Appli
40	7227	93.9	2332	4	US-10-353-753-1	Sequence 1, Appli
41	7227	93.9	2332	5	US-10-491-464-2	Sequence 2, Appli
42	7227	93.9	2332	5	US-10-938-414-2	Sequence 2, Appli
43	7227	93.9	2332	5	US-10-813-507-6	Sequence 6, Appli
44	7227	93.9	2332	5	US-10-973-941-2	Sequence 2, Appli
45	7106	92.4	1467	5	US-10-813-507-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-006-091-1
; Sequence 1, Application US/10006091
; Publication No. US20020102730A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myung-Sam
; APPLICANT: Chan, Sham-Yuen
; APPLICANT: Kelsey, William
; APPLICANT: Yee, Helena
; TITLE OF INVENTION: Expression System for Factor VIII
; FILE REFERENCE: MSB-7255.1
; CURRENT APPLICATION NUMBER: US/10/006,091
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Derived from
; OTHER INFORMATION: human factor VIII sequence
US-10-006-091-1

Query Match   99.9%; Score 7684; DB 4; Length 1438;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 1437; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 ATRRYYLGAVELSWDYMQSDLGELPVDARFPPRVPKSFPFNTSVVYKKTLFVEFTDHLFN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATRRYYLGAVELSWDYMQSDLGELPVDARFPPRVPKSFPFNTSVVYKKTLFVEFTVHLFN 60

Qy   61 IAKPRPPWMGLLGPTIQAEVYDTVVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 IAKPRPPWMGLLGPTIQAEVYDTVVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQ 120

Qy   121 REKEDDKVFPGGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 REKEDDKVFPGGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCR 180

Qy   181 EGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDRDAASARAWPKMHTVNGYVNR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDRDAASARAWPKMHTVNGYVNR 240

Qy   241 SLPGLIGCHRKSVYWHVIGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 SLPGLIGCHRKSVYWHVIGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLL 300

Qy   301 MDLGQFLLFCHISSHQHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db        301 MDLGQFLLFCHISSHQHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRF 360

Qy        361 DDDNSPSFIQIRSVAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DDDNSPSFIQIRSVAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIG 420

Qy        421 RKYKKVRFMAYTDETFKTREAIQHESGILGPLLYGEVGDTLLIIFKNQASRPYNIYPHGI 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 RKYKKVRFMAYTDETFKTREAIQHESGILGPLLYGEVGDTLLIIFKNQASRPYNIYPHGI 480

Qy        481 TDVRPLYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYYSSFVNME 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TDVRPLYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYYSSFVNME 540

Qy        541 RDLASGLIGPLLICYKESVDQRGNQIMSDKRNVILFSVFDENRSWYLTENIQRFLPNPAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 RDLASGLIGPLLICYKESVDQRGNQIMSDKRNVILFSVFDENRSWYLTENIQRFLPNPAG 600

Qy        601 VQLEDPEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKH 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VQLEDPEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKH 660

Qy        661 KMVYEDTLTLFPFSGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNTGDYYE 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 KMVYEDTLTLFPFSGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNTGDYYE 720

Qy        721 DSYEDISAYLLSKNNAIEPRSFSQNPPVLKRHQREITRTTLQSDQEEIDYDDTISVEMKK 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 DSYEDISAYLLSKNNAIEPRSFSQNPPVLKRHQREITRTTLQSDQEEIDYDDTISVEMKK 780

Qy        781 EDFDIYDEDENQSPRSFQKKTRHYFIAAVERLWDYGMSSSPHVLRNRAQSGSVPQFKKVV 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 EDFDIYDEDENQSPRSFQKKTRHYFIAAVERLWDYGMSSSPHVLRNRAQSGSVPQFKKVV 840

Qy        841 FQEFTDGSFTQPLYRGELNEHLGLLGPYIRAEVEDNIMVTFRNQASRPYSFYSSLISYEE 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 FQEFTDGSFTQPLYRGELNEHLGLLGPYIRAEVEDNIMVTFRNQASRPYSFYSSLISYEE 900

Qy        901 DQRQGAEPRKNFVKPNETKTYFWKVQHHMAPTKDEFDCKAWAYFSDVDLEKDVHSGLIGP 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 DQRQGAEPRKNFVKPNETKTYFWKVQHHMAPTKDEFDCKAWAYFSDVDLEKDVHSGLIGP 960

Qy        961 LLVCHTNTLNPAHGRQVTVQEFALFFTIFDETKSWYFTENMERNCRAPCNIQMEDPTFKE 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 LLVCHTNTLNPAHGRQVTVQEFALFFTIFDETKSWYFTENMERNCRAPCNIQMEDPTFKE 1020

Qy       1021 NYRFHAINGYIMDTLPGLVMAQDQRIRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 NYRFHAINGYIMDTLPGLVMAQDQRIRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMA 1080

Qy       1081 LYNLYPGVFETVEMLPSKAGIWRVECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRD 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 LYNLYPGVFETVEMLPSKAGIWRVECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRD 1140

Qy       1141 FQITASGQYGQWAPKLARLHYSGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFS 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 FQITASGQYGQWAPKLARLHYSGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFS 1200

Qy       1201 SLYISQFIIMYSLDGKKWQTYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 SLYISQFIIMYSLDGKKWQTYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPT 1260

Qy       1261 HYSIRSTLRMELMGCDLNSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 HYSIRSTLRMELMGCDLNSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQG 1320

Qy       1321 RSNAWRPQVNNPKEWLQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLF 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 RSNAWRPQVNNPKEWLQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLF 1380

Qy       1381 FQNGKVKVFQGNQDSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY 1438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 FQNGKVKVFQGNQDSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY 1438
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RESULT 2
US-10-047-257-1
; Sequence 1, Application US/10047257
; Publication No. US20020115152A1
; GENERAL INFORMATION:
;  APPLICANT: Cho, Myung-Sam
;  APPLICANT:  Chan, Sham-Yuen
;  APPLICANT:  Kelsey, William
;  APPLICANT:  Yee, Helena
;  TITLE OF INVENTION: Expression System for Factor VIII
;  FILE REFERENCE: MSB-7255.2
;  CURRENT APPLICATION NUMBER: US/10/047,257
;  CURRENT FILING DATE:  2002-01-15
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1438
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Derived from
;   OTHER INFORMATION: human factor VIII sequence
US-10-047-257-1

  Query Match             99.9%;  Score 7684;  DB 4;  Length 1438;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1437;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATRRYYLGAVELSWDYMQSDLGELPVDARFPPRVPKSFPFNTSVVYKKTLFVEFTDHLFN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          1 ATRRYYLGAVELSWDYMQSDLGELPVDARFPPRVPKSFPFNTSVVYKKTLFVEFTVHLFN 60

Qy         61 IAKPRPPWMGLLGPTIQAEVYDTVVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 IAKPRPPWMGLLGPTIQAEVYDTVVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQ 120

Qy        121 REKEDDKVFPGGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 REKEDDKVFPGGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCR 180

Qy        181 EGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDRDAASARAWPKMHTVNGYVNR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDRDAASARAWPKMHTVNGYVNR 240

Qy        241 SLPGLIGCHRKSVYWHVIGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SLPGLIGCHRKSVYWHVIGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLL 300

Qy        301 MDLGQFLLFCHISSHQHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 MDLGQFLLFCHISSHQHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRF 360

Qy        361 DDDNSPSFIQIRSVAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DDDNSPSFIQIRSVAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIG 420

Qy        421 RKYKKVRFMAYTDETFKTREAIQHESGILGPLLYGEVGDTLLIIFKNQASRPYNIYPHGI 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 RKYKKVRFMAYTDETFKTREAIQHESGILGPLLYGEVGDTLLIIFKNQASRPYNIYPHGI 480

Qy        481 TDVRPLYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYYSSFVNME 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TDVRPLYSRRLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYYSSFVNME 540

Qy        541 RDLASGLIGPLLICYKESVDQRGNQIMSDKRNVILFSVFDENRSWYLTENIQRFLPNPAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 RDLASGLIGPLLICYKESVDQRGNQIMSDKRNVILFSVFDENRSWYLTENIQRFLPNPAG 600

Qy        601 VQLEDPEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKH 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VQLEDPEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKH 660
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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 25, 2005, 22:47:56 ; Search time 10 Seconds
                  (without alignments)
                  435.854 Million cell updates/sec

Title: US-10-511-559-73
Perfect Score: 7693
Sequence: 1 ATRRYYLGAVELSWDYMQSD..........WVHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA_New:*
                 1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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                 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	7693	100.0	1438	1	US-10-511-559-73	Sequence 73, Appl
2	6569	85.4	1467	1	US-10-507-956-1	Sequence 1, Appli
3	1751.5	22.8	1160	1	US-10-131-826A-234	Sequence 234, App
4	261	3.4	756	1	US-10-131-826A-392	Sequence 392, App
5	217	2.8	734	1	US-10-652-893-2	Sequence 2, Appli
6	217	2.8	734	7	US-11-137-465-65	Sequence 65, Appli
7	109	1.4	1614	1	US-10-821-234-903	Sequence 903, App
8	104.5	1.4	1145	1	US-10-137-234-1432	Sequence 1432, Ap
9	104	1.4	20	1	US-10-793-626-84	Sequence 84, Appl
10	103	1.3	794	1	US-10-485-517-355	Sequence 355, App
11	98.5	1.3	501	1	US-10-511-559-84	Sequence 84, Appl
12	98	1.3	443	1	US-10-793-626-244	Sequence 244, App
13	96.5	1.3	1070	7	US/11/062	Sequence 1860, Ap
14	96.5	1.3	1095	7	US/11/062	Sequence 7, Appli
15	96	1.2	1344	7	US-11-091-643-20	Sequence 20, Appl
16	95	1.2	760	1	US-10-821-234-1141	Sequence 1141, Ap
17	95	1.2	989	1	US-10-793-626-2594	Sequence 2594, Ap
18	94.5	1.2	873	1	US-10-793-626-3036	Sequence 3036, Ap
19	91.5	1.2	477	1	US-10-793-626-3250	Sequence 3250, Ap
20	91	1.2	518	1	US-10-793-626-506	Sequence 506, App
21	91	1.2	835	1	US-10-501-039-4	Sequence 4, Appli
22	91	1.2	522	1	US-10-518-599-604	Sequence 604, App
23	90	1.2	732	1	US-10-793-626-604	Sequence 22, Appl
24	90	1.2	752	1	US-10-793-626-348	Sequence 348, App
25	89.5	1.2	1006	1	US-10-793-626-154	Sequence 154, App
26	89	1.2	619	1	US-10-821-234-1150	Sequence 1150, Ap
27	88.5	1.2	1452	1	US-10-821-234-1102	Sequence 1102, Ap
28	88.5	1.2	4384	1	US-10-821-234-1120	Sequence 1120, Ap
29	87.5	1.1	1227	1	US-10-793-626-96	Sequence 96, Appl
30	87	1.1	628	7	US-11-074-176-244	Sequence 244, App
31	86.5	1.1	687	7	US-11-074-176-260	Sequence 260, App
32	86.5	1.1	803	7	US-10-821-234-1643	Sequence 1643, Ap
33	86	1.1	15	1	US-10-511-559-81	Sequence 81, Appl
34	86	1.1	15	1	US-10-511-559-1144	Sequence 1144, Ap
35	85.5	1.1	471	7	US-10-821-234-1563	Sequence 1563, Ap
36	85.5	1.1	618	1	US-11-061-869-20	Sequence 20, Appl
37	85.5	1.1	358	1	US-10-793-626-860	Sequence 860, App
38	85	1.1	15	1	US-11-057-058-63	Sequence 63, Appli
39	84.5	1.1	1841	1	US-10-467-962B-53	Sequence 53, Appl
40	84.5	1.1	572	7	US-10-793-626-2974	Sequence 2974, Ap
41	84	1.1	849	1	US-10-511-559-374	Sequence 374, App
42	84	1.1	619	1	US-10-485-517-374	Sequence 951, App
43	83.5	1.1	919	1	US-10-821-234-951	Sequence 951, App
44	83.5	1.1	455	1	US-10-793-626-718	Sequence 718, App
45	83.5	1.1	932	7	US-11-017-550-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-10-511-559-73

; Sequence 73, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-511-559-73

Query Match   100.0%;   Score 7693;   DB 1;   Length 1438;
Best Local Similarity   100.0%;   Pred. No. 0;   Mismatches 0;
Matches 1438;   Conservative 0;   Indels 0;   Gaps 0;

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Db    1  ATRRYYLGAVELSWDYMQSDLGELPVDARFPPRVPKSFPFNTSVVYKKTLFVEFTDHLFN  60

Qy   61  IAKPRPPWMGLLGPTIQAEVYDTVVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQ  120
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Db   61  IAKPRPPWMGLLGPTIQAEVYDTVVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQ  120

Qy  121  REKEDDKVFPGGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCR  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  REKEDDKVFPGGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCR  180

Qy  181  EGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDRDAASARAWPKMHTVNGYVNR  240
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Db  181  EGSLAKEKTQTLHKFILLFAVFDEGKSWHSETKNSLMQDRDAASARAWPKMHTVNGYVNR  240

Qy  241  SLPGLIGCHRKSVYWHVIGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLL  300
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RESULT 2
US-10-507-956-1
; Sequence 1, Application US/10507956
; Publication No. US20050256038A1
; GENERAL INFORMATION:
;  APPLICANT: Societe de Conseils de Recherches et d Applications Scientifiques
;  APPLICANT: (S.C.R.A.S.)
;  TITLE OF INVENTION: Stable pharmaceutical composition containing factor VIII
;  FILE REFERENCE: 44284.M001/UMD
;  CURRENT APPLICATION NUMBER: US/10/507,956
;  CURRENT FILING DATE: 2004-09-14
;  PRIOR APPLICATION NUMBER: GB 0207092.8
;  PRIOR FILING DATE: 2003-03-26
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
;  LENGTH: 1467
;  TYPE: PRT
;  ORGANISM: Porcine
US-10-507-956-1

Query Match             85.4%;  Score 6569;  DB 1;  Length 1467;
Best Local Similarity   83.7%;  Pred. No. 0;
Matches 1213;  Conservative 106;  Mismatches 118;  Indels 12;  Gaps 3;
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Qy      1 ATRRYYLGAVELSWDYMQSD-LGELPVDARFPPRVPKSFPFNTSVVYKKTLFVEFTDHLF 59
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Db     20 AIRRYYLGAVELSWDYRQSELLRELHVDTRFPATAPGALPLGPSVLYKKTVVFEFTDQLF 79

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Qy    120 QREKEDDKVFPGGSHTYVWQVLKENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVC 179
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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: November 25, 2005, 23:18:02 ; Search time 1.13793 Seconds
(without alignments)
39.954 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect Score: 75
Sequence: 1 MSSSPHVLRNRAOSG 15
Searched: 17545 seqs, 3030971 residues
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%, Maximum Match 100%, Listing first 1000 summaries

Database :
Published Applications AA_New:*
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2: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	DB	DB ID	Description
1	75	100.0	15	1	US-10-511-559-80	Sequence 80, Appl1
2	75	100.0	1438	1	US-10-511-559-73	Sequence 73, Appl1
3	65	86.7	13	1	US-10-511-559-831	Sequence 831, Appl1
4	64	85.3	13	1	US-10-511-559-832	Sequence 832, App
5	58	77.3	13	1	US-10-511-559-833	Sequence 833, App
6	56	74.7	13	1	US-10-511-559-830	Sequence 830, App
7	56	74.7	1467	1	US-10-507-956-1	Sequence 1, Appli
8	51	68.0	13	1	US-10-511-559-834	Sequence 834, App
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12	37	49.3	534	1	US-10-821-234-1341	Sequence 1341, Ap
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16	33	44.0	826	1	US-10-821-234-1048	Sequence 1048, Ap
17	32	42.7	13	1	US-10-511-559-826	Sequence 826, App
18	32	42.7	119	1	US-10-793-626-1372	Sequence 1372, Ap
19	32	42.7	240	1	US-10-689-742-210	Sequence 210, App
20	32	42.7	314	1	US-10-995-793-74	Sequence 74, Appl
21	32	42.7	555	1	US-10-131-826A-72	Sequence 72, Appli
22	32	42.7	284	1	US-10-518-599-2	Sequence 2, Appli
23	31	41.3	289	1	US-10-793-626-3254	Sequence 3254, Ap
24	31	41.3	379	1	US-10-632-150-6	Sequence 6, Appli
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26	31	41.3	434	1	US-10-632-150-24	Sequence 24, Appl1
27	31	41.3	616	7	US-10-131-826A-206	Sequence 206, Appl
28	31	41.3	709	7	US-11-074-176-158	Sequence 158, App
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43	29	38.7	337	1	US-10-821-234-1004	Sequence 1004, Ap
44	29	38.7	361	1	US-10-793-626-1914	Sequence 1914, Ap
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48	29	38.7	513	7	US-10-485-517-326	Sequence 326, App
49	29	38.7	849	7	US-10-485-517-179	Sequence 179, App
50	29	38.7	513	7	US-10-485-517-366	Sequence 366, App
51	29	38.7	119	7	US-10-858-730-710	Sequence 710, App
52	29	38.7	2335	7	US-11-056-354-2	Sequence 2, Appli
53	29	38.7	883	1	US-10-467-962B-53	Sequence 53, Appl
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55	29	38.7	116	7	US-10-793-626-2964	Sequence 2964, Ap
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57	28	37.3	196	1	US-10-821-234-1486	Sequence 1486, Ap
58	28	37.3	272	7	US-10-793-626-732	Sequence 732, App
59	28	37.3	286	7	US-11-082-389-88	Sequence 88, Appl
60	28	37.3	311	7	US-10-793-626-2460	Sequence 2460, Ap
61	28	37.3	328	1	US-10-131-826A-34	Sequence 34, Appl
62	28	37.3	342	1	US-10-131-386-40	Sequence 40, Appl
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81	27	36.0	284	7	US-11-074-176-254	Sequence 254, App
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83	27	36.0	299	7	US-10-793-626-1324	Sequence 1324, Ap
84	27	36.0	301	7	US-11-074-176-362	Sequence 362, App
85	27	36.0	308	7	US-11-082-389-140	Sequence 140, App
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91	27	36.0	354	1	US-10-485-517-366	Sequence 366, App
92	27	36.0	373	7	US-10-793-626-2774	Sequence 2774, Ap
93	27	36.0	374	7	US-10-821-234-1072	Sequence 1072, Ap
94	27	36.0	400	1	US-10-793-626-2774	Sequence 2774, Ap
95	27	36.0	400	1	US-10-858-730-204	Sequence 204, App
96	27	36.0	432	7	US-11-056-354-4	Sequence 4, Appli
97	27	36.0	432	1	US-10-821-234-1606	Sequence 1606, Ap
98	27	36.0	480	1	US-10-821-234-1465	Sequence 1465, Ap

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99	27	36.0	510	1	US-10-793-626-2860	Sequence 2860, Ap
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102	27	36.0	696	7	US-11-131-826A-354	Sequence 354, App
103	27	36.0	697	1	US-11-074-176-150	Sequence 150, App
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105	27	36.0	761	1	US-10-485-517-252	Sequence 252, App
106	27	36.0	903	1	US-10-689-742-142	Sequence 142, App
107	27	36.0	1126	1	US-10-485-517-248	Sequence 248, App
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114	27	34.7	1058	1	US-10-821-234-1473	Sequence 1473, Ap
115	27	34.7	33	1	US-10-986-501-268	Sequence 268, App
116	27	34.7	85	7	US-11-082-544-31	Sequence 31, Appl
117	27	34.7	135	1	US-10-821-234-1037	Sequence 1037, Ap
118	27	34.7	160	1	US-11-054-515-1273	Sequence 1273, Ap
119	27	34.7	161	1	US-10-467-962B-67	Sequence 67, Appl
120	27	34.7	202	1	US-10-980-388-109	Sequence 109, App
121	27	34.7	222	1	US-10-793-626-376	Sequence 376, App
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125	27	34.7	242	1	US-10-821-234-1073	Sequence 1073, Ap
126	27	34.7	248	1	US-11-054-515-1273	Sequence 1273, Ap
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128	27	34.7	254	1	US-10-793-626-902	Sequence 902, App
129	27	34.7	264	1	US-10-793-626-776	Sequence 776, App
130	27	34.7	267	1	US-10-627-952-20	Sequence 20, Appl
131	27	34.7	271	1	US-10-667-295-98	Sequence 98, Appl
132	27	34.7	272	1	US-10-986-501-120	Sequence 120, App
133	27	34.7	277	1	US-10-667-295-97	Sequence 97, Appl
134	27	34.7	282	1	US-10-972-587-28	Sequence 28, Appl
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136	27	34.7	296	1	US-10-667-295-96	Sequence 96, Appl
137	27	34.7	327	1	US-10-821-234-1686	Sequence 1686, Ap
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139	27	34.7	339	7	US-10-874-15	Sequence 15, Appl
140	27	34.7	342	1	US-11-152-892-11	Sequence 11, Appl
141	27	34.7	358	1	US-10-793-626-918	Sequence 918, App
142	27	34.7	361	1	US-10-793-626-160	Sequence 160, App
143	27	34.7	399	1	US-11-018-018-3	Sequence 3, Appli
144	27	34.7	399	7	US-10-047-757-3	Sequence 3, Appli
145	27	34.7	400	1	US-10-821-234-1534	Sequence 1534, Ap
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147	27	34.7	490	1	US-10-131-826A-356	Sequence 356, App
148	27	34.7	516	1	US-10-486-968-52	Sequence 52, Appl
149	27	34.7	540	1	US-10-821-234-1456	Sequence 1456, Ap
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153	27	34.7	839	1	US-10-821-234-955	Sequence 955, App
154	27	34.7	1094	1	US-10-821-234-1097	Sequence 1097, Ap
155	27	34.7	1122	1	US-10-821-234-1657	Sequence 1657, Ap
156	27	34.7	1127	1	US-11-096-051-13	Sequence 13, Appl
157	27	34.7	1187	1	US-10-821-234-1262	Sequence 1262, Ap
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175	25.5	34.0	829	7	US-10-512-109-27	Sequence 27, Appl
176	25.5	34.0	832	1	US-10-512-109-29	Sequence 29, Appl
177	25	33.3	32	1	US-10-986-501-153	Sequence 153, App
178	25	33.3	34	7	US-10-793-626-1576	Sequence 1576, Ap
179	25	33.3	91	7	US-10-821-234-1474	Sequence 1474, Ap
180	25	33.3	101	7	US-10-510-386-170	Sequence 170, App
181	25	33.3	143	1	US-10-510-386-130	Sequence 130, App
182	25	33.3	143	1	US-10-793-626-1018	Sequence 1018, Ap
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191	25	33.3	224	7	US-10-977-334-6	Sequence 6, Appl
192	25	33.3	230	1	US-10-793-626-632	Sequence 632, App
193	25	33.3	230	1	US-10-793-626-2720	Sequence 2720, Ap
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203	25	33.3	371	1	US-10-131-826A-216	Sequence 216, App
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265	24	32.0	142	1	US-11-013-247A-11	Sequence 11, Appl
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314	24	32.0	395	7	US-11-074-176-188	Sequence 188, App
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356	24	32.0	763	7	US-11-013-247A-35	Sequence 35, Appli
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452	23	30.7	163	1	US-10-821-234-2330	Sequence 2330, Ap
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485	23	30.7	237	1	US-10-793-626-3244	Sequence 3244, Ap
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487	23	30.7	249	1	US-11-074-176-116	Sequence 116, App
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499	23	30.7	263	1	US-10-821-234-1403	Sequence 1403, Ap
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950	22	29.3	146	1	US-10-835-615-721	Sequence 721, App
951	22	29.3	146	1	US-10-835-615-723	Sequence 723, App
952	22	29.3	146	1	US-10-835-615-725	Sequence 725, App
953	22	29.3	146	1	US-10-835-615-727	Sequence 727, App
954	22	29.3	146	1	US-10-835-615-729	Sequence 729, App
955	22	29.3	146	1	US-10-835-615-731	Sequence 731, App
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958	22	29.3	146	1	US-10-835-615-737	Sequence 737, App
959	22	29.3	146	1	US-10-835-615-739	Sequence 739, App
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992	22	29.3	146	1	US-10-835-615-823	Sequence 823, App
993	22	29.3	146	1	US-10-835-615-825	Sequence 825, App
994	22	29.3	146	1	US-10-835-615-833	Sequence 833, App
995	22	29.3	146	1	US-10-835-615-835	Sequence 835, App
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998	22	29.3	146	1	US-10-835-615-841	Sequence 841, App
999	22	29.3	146	1	US-10-835-615-843	Sequence 843, App
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ALIGNMENTS

RESULT 1
US-10-511-559-80
; Sequence 80, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Epitope of human Factor VIII
US-10-511-559-80

Query Match   100.0%; Score 75; DB 1; Length 15;
Best Local Similarity   100.0%; Pred. No. 4.3e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MSSSPHVLRNRAQSG 15
          |||||||||||||||
Db   1 MSSSPHVLRNRAQSG 15

RESULT 2
US-10-511-559-73
; Sequence 73, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
;
;

; SEQ ID NO 73
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-511-559-73

Query Match   100.0%; Score 75; DB 1; Length 1438;
Best Local Similarity   100.0%; Pred. No. 8.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MSSSPHVLRNRAQSG 15
          |||||||||||||||
Db   817 MSSSPHVLRNRAQSG 831

RESULT 3
US-10-511-559-831
; Sequence 831, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 831
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-831

Query Match   86.7%; Score 65; DB 1; Length 13;
Best Local Similarity   100.0%; Pred. No. 2.8e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MSSSPHVLRNRAQ 13
          |||||||||||||
Db   1 MSSSPHVLRNRAQ 13

RESULT 4
US-10-511-559-832
; Sequence 832, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: November 25, 2005, 23:10:10 ; Search time 29.6897 Seconds
(without alignments)
211.098 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect Score: 75
Sequence: 1 MSSSPHVLRNRAOSG 15

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :   Published Applications AA_Main:*
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                6: /cgn2_6/ptcodata/1/pubpaa/US11_PUBCOMB.pep:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	75	100.0	15	6	US-11-009-460-109	Sequence 109, Appl
2	75	100.0	20	4	US-10-433-273-59	Sequence 59, Appl
3	75	100.0	60	4	US-10-472-516-5	Sequence 4, Appli
4	75	100.0	1424	5	US-10-968-286-5	Sequence 5, Appli
5	75	100.0	1424	5	US-10-006-091-1	Sequence 1, Appli
6	75	100.0	1438	4	US-10-047-257-1	Sequence 1, Appli
7	75	100.0	1438	4	US-10-225-900-1	Sequence 1, Appli
8	75	100.0	1438	4	US-10-813-507-13	Sequence 13, Appl
9	75	100.0	1457	5	US-10-813-507-17	Sequence 17, Appl
10	75	100.0	1457	4	US-10-239-498A-4	Sequence 4, Appl
11	75	100.0	1459	4	US-10-239-498A-13	Sequence 13, Appl
12	75	100.0	1459	4	US-10-239-498A-15	Sequence 15, Appl
13	75	100.0	1471	4	US-10-095-718-2	Sequence 2, Appli
14	75	100.0	1471	5	US-10-681-970-2	Sequence 2, Appli
15	75	100.0	2096	4	US-10-741-600-1032	Sequence 1032, Ap
16	75	100.0	2096	3	US-09-957-641-2	Sequence 2, Appli
17	75	100.0	2332	4	US-10-187-319-2	Sequence 2, Appli
18	75	100.0	2332	4	US-10-131-510A-2	Sequence 2, Appli
19	75	100.0	2332	4	US-10-445-235-2	Sequence 2, Appli
20	75	100.0	2332	4	US-10-360-101-229	Sequence 229, App
21	75	100.0	2332	4	US-10-960-286-2	Sequence 2, Appli
22	75	100.0	2332	4	US-10-492-261-30	Sequence 30, Appl
23	75	100.0	2332	4	US-10-095-718-4	Sequence 4, Appli
24	75	100.0	2332	4	US-10-085-196-168	Sequence 168, App
25	75	100.0	2332	5	US-10-721-997A-34	Sequence 34, Appl
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28	75	100.0	2332	5	US-10-938-414-2	Sequence 8, Appli
29	75	100.0	2332	5	US-10-813-507-6	Sequence 6, Appli
30	75	100.0	2332	4	US-10-973-941-2	Sequence 2, Appli
31	75	100.0	2351	4	US-10-132-829-4	Sequence 4, Appli
32	75	100.0	2351	4	US-10-172-712-27	Sequence 27, Appli
33	75	100.0	2351	4	US-10-789-955-1	Sequence 1, Appli
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44	75	100.0	2351	5	US-10-410-980-30	Sequence 30, Appl
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49	75	92.0	1431	5	US-10-492-261-30	Sequence 30, Appl
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53	75	74.7	1443	4	US-10-131-510A-37	Sequence 37, Appli
54	75	74.7	1443	5	US-10-491-464-37	Sequence 37, Appl
55	75	74.7	1467	4	US-10-938-414-39	Sequence 39, Appl
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57	75	74.7	1467	4	US-10-811-507-15	Sequence 15, Appl
58	75	74.7	1467	5	US-10-187-319-39	Sequence 39, Appli
59	75	74.7	2114	4	US-10-973-941-3	Sequence 3, Appl
60	75	74.7	2114	4	US-10-721-997A-33	Sequence 33, Appl
61	75	74.7	2133	4	US-10-437-963-104573	Sequence 104573, Appl
62	75	74.7	2133	5	US-10-437-963-104573	Sequence 104573, Appl
63	75	74.7	2133	5	US-10-424-599-278179	Sequence 278179, Appl
64	75	74.7	2133	4	US-10-424-599-278182	Sequence 278182, Appl
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66	75	60.0	20	4	US-10-732-923-9907	Sequence 9907, A
67	75	57.3	1561	4	US-10-425-114-44463	Sequence 44463, A
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69	75	57.3	2319	4	US-10-425-115-367215	Sequence 367215, A
70	75	57.3	2319	4	US-09-768-762-84	Sequence 84, Appl
71	75	57.3	2319	5	US-10-289-762-42	Sequence 42, Appl
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73	75	54.7	46	4	US-10-491-464-6	GENERAL INFORMA
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75	75	53.3	168	4	US-10-131-510A-6	Sequence 15, Appl
76	75	53.3	277	4	US-10-874-486-54	Sequence 54, Appl
77	75	53.3	382	4	US-09-768-826-54	Sequence 54, Appl
78	75	53.3	444	5	US-10-874-486-54	Sequence 54, Appl
79	75	53.3	462	4	US-09-768-826-54	Sequence 54, Appl
80	75	52.7	836	4	US-10-681-970-2	Sequence 2, Appli
81	75	52.0	84	4	US-10-450-763-36719	Sequence 36719, A
82	75	52.0	93	4	US-10-450-763-182742	Sequence 182742, A
83	75	52.0	131	4	US-10-437-963-182742	Sequence 182742, A
84	75	52.0	251	4	US-10-450-763-43346	Sequence 43946, A
85	75	52.0	251	3	US-10-756-149-4932	Sequence 4932, Ap
86	75	52.0	251	3	US-10-437-963-129936	Sequence 129936, A
87	75	52.0	314	3	US-10-963-129936	Sequence 12936, Ap
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89	75	52.0	324	4	US-10-492-032-8	Sequence 8, Appli
90	75	52.0	347	4	US-10-437-963-51964	Sequence 51964, A
91	75	52.0	405	4	US-10-450-763-51964	Sequence 51964, A
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94	75	52.0	473	5	US-10-450-763-51961	Sequence 51961, A
95	75	52.0	562	4	US-10-437-763-51961	Sequence 51961, A
96	75	52.0	666	4	US-10-763-52182	Sequence 52182, A
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104	38	50.7	97	4	US-10-437-963-102788	Sequence 102788,
105	38	50.7	134	4	US-10-425-115-341173	Sequence 341173,
106	38	50.7	223	4	US-10-425-114-65802	Sequence 65802, A
107	38	50.7	226	4	US-10-425-115-325321	Sequence 325321,
108	38	50.7	245	4	US-10-425-115-325320	Sequence 325320,
109	38	50.7	264	4	US-10-425-114-51597	Sequence 51597, A
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115	38	50.7	433	4	US-10-389-640-17	Sequence 17, Appl
116	38	50.7	514	4	US-10-467-758-2	Sequence 2, Appli
117	38	50.7	598	4	US-10-425-115-187115	Sequence 187115,
118	38	50.7	983	6	US-11-097-143-37182	Sequence 37182, A
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122	38	50.7	2414	4	US-10-473-127-641	Sequence 641, App
123	38	50.7	2414	4	US-10-473-127-644	Sequence 644, App
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151	37	49.3	245	6	US-11-097-143-2358	Sequence 2358, Ap
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638	33	44.0	182	4	US-10-156-761-8557	Sequence 8557, A
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642	33	44.0	193	4	US-10-092-947A-4	Sequence 4, Appl
643	33	44.0	199	4	US-10-424-599-12997	Sequence 12997, A
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645	33	44.0	202	4	US-10-739-930-10893	Sequence 10893, A
646	33	44.0	203	4	US-10-767-701-35396	Sequence 35396, A
647	33	44.0	204	4	US-10-425-115-276214	Sequence 276214,
648	33	44.0	205	4	US-10-108-260A-4682	Sequence 4682, Ap
649	33	44.0	208	4	US-10-250-615-7	Sequence 7, Appl
650	33	44.0	209	4	US-10-425-115-357094	Sequence 357094,
651	33	44.0	212	4	US-10-437-963-174010	Sequence 174010, A
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659	33	44.0	229	4	US-10-369-493-16463	Sequence 16463, A
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663	33	44.0	244	4	US-10-425-115-240751	Sequence 240751,
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667	33	44.0	252	4	US-10-767-701-39311	Sequence 39311, A
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671	33	44.0	254	3	US-09-764-864-1157	Sequence 1157, Ap
672	33	44.0	254	4	US-10-097-143-40473	Sequence 40473, Ap
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688	33	44.0	298	3	US-09-815-242-11690	Sequence 11690, A
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696	33	44.0	298	4	US-10-282-122A-76223	Sequence 76223, A
697	33	44.0	298	4	US-10-282-122A-77746	Sequence 77746, A
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704	33	44.0	307	4	US-10-306-762-129	Sequence 129, App
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707	33	44.0	309	4	US-10-412-699B-150	Sequence 150, App
708	33	44.0	310	4	US-10-282-122A-51206	Sequence 51206, A
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716	33	44.0	331	4	US-10-369-493-6216	Sequence 6216, Ap
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722	33	44.0	351	4	US-10-732-923-5975	Sequence 5975, Ap
723	33	44.0	353	4	US-10-282-122A-38412	Sequence 38412, Ap
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743	33	44.0	388	4	US-10-157-031-123	Sequence 123, App
744	33	44.0	388	4	US-10-157-031-124	Sequence 124, App
745	33	44.0	388	4	US-10-225-567A-18	Sequence 18, App
746	33	44.0	388	4	US-10-925-095-439	Sequence 439, App
747	33	44.0	388	4	US-10-481-029-142	Sequence 142, App
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798	33	44.0	549	4	US-10-166-192-24	Sequence 24, Appl
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805	33	44.0	555	3	US-09-764-864-1161	Sequence 1161, Ap
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808	33	44.0	568	4	US-10-094-749-2562	Sequence 2562, Ap
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823	33	44.0	657	4	US-10-389-566-1439	Sequence 1439, Ap
824	33	44.0	657	4	US-10-425-114-64717	Sequence 64717, A
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833	33	44.0	707	4	US-10-225-486-57	Sequence 57, Appl
834	33	44.0	707	5	US-10-494-905-50	Sequence 50, Appl
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843	33	44.0	797	4	US-10-369-493-5150	Sequence 5150, Ap
844	33	44.0	798	5	US-10-489-740-148	Sequence 148, Appl
845	33	44.0	819	4	US-10-108-260A-3302	Sequence 3302, Ap
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847	33	44.0	822	4	US-10-450-763-48171	Sequence 48171, A
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854	33	44.0	859	4	US-10-433-544-10	Sequence 10, Appl
855	33	44.0	860	4	US-10-128-714-8444	Sequence 8444, Ap
856	33	44.0	862	4	US-10-275-762-6	Sequence 6, Appli
857	33	44.0	862	4	US-10-275-762-3	Sequence 3, Appli
858	33	44.0	862	5	US-10-494-940-51	Sequence 51, Appl
859	33	44.0	863	4	US-10-295-027-1229	Sequence 1229, Ap
860	33	44.0	874	5	US-10-450-763-32592	Sequence 32592, A
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862	33	44.0	887	4	US-10-174-677-42	Sequence 42, Appl
863	33	44.0	889	4	US-10-187-975-28	Sequence 28, Appl
864	33	44.0	889	4	US-10-450-763-43330	Sequence 43330, A
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867	33	44.0	898	6	US-11-097-143-23934	Sequence 23934, A
868	33	44.0	902	4	US-10-275-762-5	Sequence 5, Appli
869	33	44.0	902	4	US-10-024-298A-156	Sequence 156, App
870	33	44.0	912	4	US-10-042-211A-156	Sequence 156, App
871	33	44.0	912	4	US-10-617-217A-156	Sequence 156, App
872	33	44.0	912	4	US-10-024-298A-156	Sequence 156, App
873	33	44.0	912	4	US-10-174-677-100	Sequence 100, App
874	33	44.0	938	6	US-11-097-143-23934	Sequence 23934, A
875	33	44.0	941	4	US-10-097-143-24087	Sequence 24087, A
876	33	44.0	941	6	US-11-097-143-337013	Sequence 337013,
877	33	44.0	959	4	US-10-425-115-337013	Sequence 337013,
878	33	44.0	967	4	US-10-275-762-77	Sequence 77, Appl
879	33	44.0	968	4	US-10-275-762-10	Sequence 10, Appl
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881	33	44.0	1006	4	US-10-024-298A-158	Sequence 158, App
882	33	44.0	1006	4	US-10-042-211A-158	Sequence 158, App
883	33	44.0	1006	4	US-10-617-217A-158	Sequence 158, App
884	33	44.0	1006	4	US-10-408-755A-2710	Sequence 2710, Ap
885	33	44.0	1006	4	US-10-024-298A-158	Sequence 158, App
886	33	44.0	1039	4	US-10-174-677-100	Sequence 100, App
887	33	44.0	1039	6	US-11-097-143-23934	Sequence 23934, A
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889	33	44.0	1041	5	US-10-097-143-24087	Sequence 24087, A
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ALIGNMENTS

RESULT 1
US-11-009-460-109
Sequence 109, Application US/11009460
Publication No. US20050181459A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: METHOD FOR MAPPING AND ELIMINATING
; TITLE OF INVENTION: T-CELL EPITOPES
; FILE REFERENCE: MER-135
; CURRENT APPLICATION NUMBER: US/11/009,460
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: PCT/EP03/06110
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: EP02012919.3
; PRIOR FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential T-cell Epitopes
US-11-009-460-109

Query Match 100.0%; Score 75; DB 6; Pred. No. 2e-06; Length 15;
Best Local Similarity 100.0%;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   1  MSSSPHVLRNRAQSG 15
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RESULT 2
US-10-433-273-59
Sequence 59, Application US/10433273
Publication No. US20040096456A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; APPLICANT: Conti-Fine, Bianca M.
; TITLE OF INVENTION: Methods to Treat Hemophilia
; FILE REFERENCE: 600.507W01
; CURRENT APPLICATION NUMBER: US/10/433,273
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US 60/250,430
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 59
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-433-273-59

Query Match 100.0%; Score 75; DB 4; Pred. No. 2.7e-06; Length 20;
Best Local Similarity 100.0%;
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RESULT 3
US-10-433-273-4
Sequence 4, Application US/10433273
Publication No. US20040096456A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; APPLICANT: Conti-Fine, Bianca M.
; TITLE OF INVENTION: Methods to Treat Hemophilia
; FILE REFERENCE: 600.507W01
; CURRENT APPLICATION NUMBER: US/10/433,273
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US 60/250,430
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 4
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-433-273-4

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Best Local Similarity 100.0%;
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RESULT 4
US-10-472-516-5
Sequence 5, Application US/10472516
Publication No. US20040248785A1
; GENERAL INFORMATION:
; APPLICANT: Saenko, Evgueni L.
; APPLICANT: Sarafanov, Andrey G.
; TITLE OF INVENTION: Methods and Compositions for Reducing Heparan Sulfate
; TITLE OF INVENTION: Proteoglycan-Mediated Clearance of Factor VIII
; FILE REFERENCE: 1327.0660001
; CURRENT APPLICATION NUMBER: US/10/472,516
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: PCT/US02/00583
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/260,904
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 1424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-472-516-5

OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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96	35	46.7	147	2	US-08-120-211A-834	Sequence 834, Appl
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101	35	46.7	206	2	US-09-248-796A-14366	Sequence 14366, A
102	35	46.7	300	2	US-09-902-540-11871	Sequence 11871, A
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105	35	46.7	345	1	US-07-954-840A-10	Sequence 10, Appl
106	35	46.7	345	1	US-07-954-840A-12	Sequence 12, Appl
107	35	46.7	345	1	US-07-954-840A-14	Sequence 14, Appl
108	35	46.7	345	1	US-07-954-840A-16	Sequence 16, Appl
109	35	46.7	345	1	US-07-954-840A-18	Sequence 18, Appl
110	35	46.7	345	1	US-07-954-840A-20	Sequence 20, Appl
111	35	46.7	345	1	US-07-954-840A-22	Sequence 22, Appl
112	35	46.7	345	1	US-07-954-840A-24	Sequence 24, Appl
113	35	46.7	345	1	US-07-954-840A-26	Sequence 26, Appl
114	35	46.7	345	1	US-07-954-840A-31	Sequence 31, Appl
115	35	46.7	347	1	US-07-954-840A-4	Sequence 4, Appli
116	35	46.7	347	1	US-07-954-840A-6	Sequence 6, Appli
117	35	46.7	347	1	US-07-954-840A-28	Sequence 28, Appl
118	35	46.7	347	1	US-07-954-840A-29	Sequence 29, Appl
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121	35	46.7	388	2	US-09-134-001C-4951	Sequence 4951, Ap
122	35	46.7	397	2	US-09-270-767-46699	Sequence 46699, A
123	35	46.7	463	2	US-09-489-039A-9034	Sequence 9034, Ap
124	35	46.7	484	2	US-09-489-039A-19783	Sequence 19783, A
125	35	46.7	585	1	US-08-453-848-11	Sequence 11, Appl
126	35	46.7	586	1	US-09-169-027-19	Sequence 19, Appl
127	35	46.7	586	1	US-08-453-848-19	Sequence 19, Appl
128	35	46.7	592	1	US-08-453-848-17	Sequence 17, Appl
129	35	46.7	592	1	US-09-169-027-17	Sequence 17, Appl
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133	35	46.7	1784	2	US-08-652-426A-2	Sequence 2, Appli
134	35	46.7	1784	2	US-09-949-016-8283	Sequence 8283, Ap
135	35	46.7	1813	2	US-09-949-016-8284	Sequence 8284, Ap
136	35	46.7	1813	2	US-09-949-016-8285	Sequence 8285, Ap
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154	34	45.3	392	2	US-09-605-703B-1682	Sequence 1682, Ap
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162	34	45.3	459	1	US-08-673-312-2	Sequence 2, Appli
163	34	45.3	500	1	US-07-755-573C-8	Sequence 8, Appli
164	34	45.3	502	1	US-08-519-878-2	Sequence 2, Appli
165	34	45.3	502	2	US-09-902-540-13393	Sequence 13393, A
166	34	45.3	518	2	US-09-252-991A-23604	Sequence 23604, A
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168	34	45.3	589	2	US-09-453-848-13	Sequence 13, Appl
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171	34	45.3	715	2	US-10-104-047-3385	Sequence 3385, Ap
172	34	45.3	740	2	US-09-022-983-5	Sequence 5, Appli
173	34	45.3	742	2	US-09-949-016-11569	Sequence 11569, A

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174	34	45.3	1025	2	US-09-543-681A-7112	Sequence 7112, Ap
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176	34	45.3	1182	2	US-09-060-932A-7	Sequence 7, Appli
177	34	45.3	1213	1	US-08-188-582-20	Sequence 20, Appl
178	34	45.3	1213	2	US-08-646-715-20	Sequence 20, Appl
179	34	45.3	1430	2	US-09-252-991A-18190	Sequence 18190, A
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181	34	44.7	102	2	US-09-634-238-347	Sequence 347, App
182	34	44.0	118	2	US-09-270-767-61948	Sequence 61948, A
183	34	44.0	170	2	US-09-513-999C-5046	Sequence 5046, Ap
184	34	44.0	170	2	US-09-513-999C-5047	Sequence 5047, Ap
185	34	44.0	193	2	US-09-270-767-46373	Sequence 46373, A
186	34	44.0	209	2	US-09-270-767-46539	Sequence 46539, A
187	34	44.0	227	2	US-09-711-164-352	Sequence 352, App
188	34	44.0	291	2	US-09-252-991A-32503	Sequence 32503, A
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195	34	44.0	377	2	US-07-996-772A-4	Sequence 4, Appli
196	33	44.0	377	1	US-08-446-822-4	Sequence 4, Appli
197	33	44.0	377	1	US-08-480-888B-6	Sequence 6, Appli
198	33	44.0	382	2	US-08-220-401-4	Sequence 4, Appli
199	33	44.0	388	2	US-08-437-362-4	Sequence 4, Appli
200	33	44.0	388	2	US-08-360-606B-30	Sequence 30, Appl
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213	33	44.0	492	2	US-10-104-047-3223	Sequence 3223, Ap
214	33	44.0	497	2	US-10-104-047-3223	Sequence 3223, Ap
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232	33	44.0	997	2	US-08-428-948A-1	Sequence 1, Appli
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234	33	44.0	998	4	PCT-US95-04655-1	Sequence 1, Appli
235	33	44.0	1021	2	US-08-233-008A-6	Sequence 6, Appli
236	33	44.0	1082	2	US-09-531-092-533	Sequence 533, App
237	33	44.0	1268	2	US-09-270-767-45320	Sequence 45320, A
238	33	44.0	1326	2	US-09-949-016-6806	Sequence 6806, Ap
239	33	44.0	1339	2	US-09-270-767-6806	Sequence 6806, Ap
240	33	44.0	1463	2	US-08-220-603A-11	Sequence 11, Appl
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243	33	44.0	1712	2	US-09-949-016-9450	Sequence 9450, Ap
244	32	44.0	18	2	US-09-322-352-7347	Sequence 7347, Ap
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246	32	42.7	34	1	US-08-457-616-16	Sequence 16, Appl

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249	32	42.7	100	2	US-09-732-210-1166	Sequence 1166, Ap
250	32	42.7	106	2	US-09-248-796A-14408	Sequence 14408, A
251	32	42.7	118	2	US-09-134-001C-5272	Sequence 5272, Ap
252	32	42.7	119	2	US-09-710-279-1372	Sequence 1372, Ap
253	32	42.7	161	2	US-09-252-991A-28006	Sequence 28006, A
254	32	42.7	162	2	US-10-104-047-3256	Sequence 3256, Ap
255	32	42.7	167	2	US-09-902-540-10299	Sequence 10299, A
256	32	42.7	171	2	US-09-270-767-32338	Sequence 32338, A
257	32	42.7	233	2	US-09-270-767-47555	Sequence 47555, A
258	32	42.7	233	2	US-09-311-021-46	Sequence 46, Appl
259	32	42.7	239	2	US-08-634-475-4	Sequence 4, Appli
260	32	42.7	239	2	US-09-709-791-5	Sequence 5, Appli
261	32	42.7	240	2	US-09-978-248A-5	Sequence 5, Appli
262	32	42.7	243	2	US-08-634-475-5	Sequence 5, Appli
263	32	42.7	243	2	US-09-709-791-4	Sequence 4, Appli
264	32	42.7	255	2	US-07-795-859B-2	Sequence 2, Appli
265	32	42.7	255	1	US-08-457-616-2	Sequence 2, Appli
266	32	42.7	259	1	US-07-795-859B-4	Sequence 4, Appli
267	32	42.7	259	1	US-08-457-616-4	Sequence 4, Appli
268	32	42.7	279	2	US-09-270-767-61577	Sequence 61577, A
269	32	42.7	284	2	US-09-270-767-58734	Sequence 58734, A
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271	32	42.7	288	2	US-09-949-016-11404	Sequence 11404, A
272	32	42.7	289	2	US-09-328-352-7971	Sequence 7971, Ap
273	32	42.7	290	2	US-09-068-804-40	Sequence 40, Appl
274	32	42.7	290	4	US-09-068-804-5	Sequence 5, Appl
275	32	42.7	301	2	PCT-US93-08528-39	Sequence 39, Appl
276	32	42.7	308	2	US-09-270-767-62218	Sequence 62218, A
277	32	42.7	317	2	US-09-252-991A-26226	Sequence 26226, A
278	32	42.7	319	2	US-09-188-930-184	Sequence 184, App
279	32	42.7	321	2	US-09-312-283C-184	Sequence 184, App
280	32	42.7	321	2	US-09-252-991A-24630	Sequence 24630, A
281	32	42.7	326	1	US-08-118-270-39	Sequence 39, Appl
282	32	42.7	326	4	US-09-489-039A-13753	Sequence 13753, A
283	32	42.7	328	2	US-09-328-352-7662	Sequence 7662, Ap
284	32	42.7	336	2	US-09-543-681A-4292	Sequence 4292, Ap
285	32	42.7	340	2	US-09-270-767-33569	Sequence 33569, A
286	32	42.7	343	2	US-09-252-991A-15519	Sequence 15519, A
287	32	42.7	349	2	US-09-338-671-4	Sequence 4, Appli
288	32	42.7	357	2	US-09-615-192A-323	Sequence 323, App
289	32	42.7	362	2	US-09-252-991A-21176	Sequence 21176, A
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291	32	42.7	368	2	US-09-252-991A-18062	Sequence 18062, A
292	32	42.7	370	2	US-09-144-914-8	Sequence 8, Appli
293	32	42.7	370	2	US-09-655-272-4	Sequence 4, Appli
294	32	42.7	374	2	US-09-540-236-2230	Sequence 2230, Ap
295	32	42.7	393	2	US-08-178-257-17	Sequence 17, Appl
296	32	42.7	397	2	US-09-377-557-14	Sequence 14, Appl
297	32	42.7	403	2	US-09-602-787A-606	Sequence 606, App
298	32	42.7	408	2	US-09-248-796A-1907	Sequence 1907, Ap
299	32	42.7	411	2	US-09-236-080-6	Sequence 6, Appli
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319	32	42.7	519	2	US-09-162-368B-2	Sequence 2, Appli

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323	32	42.7	550	2	US-09-252-991A-20120	Sequence 20120, A
324	32	42.7	550	2	US-09-949-016-9886	Sequence 9886, Ap
325	32	42.7	564	2	US-09-252-991A-26890	Sequence 26890, A
326	32	42.7	576	2	US-09-248-796A-20352	Sequence 20352, A
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330	32	42.7	593	2	US-09-614-912-90	Sequence 90, Appl
331	32	42.7	627	2	US-09-538-106-22	Sequence 22, Appl
332	32	42.7	680	2	US-09-538-116-19	Sequence 19, Appl
333	32	42.7	681	2	US-10-158-847-140	Sequence 140, App
334	32	42.7	681	2	US-10-158-825-140	Sequence 140, App
335	32	42.7	694	2	US-09-248-796A-20618	Sequence 20618, A
336	32	42.7	711	2	US-10-158-847-138	Sequence 138, App
337	32	42.7	711	2	US-10-158-825-138	Sequence 138, App
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342	32	42.7	744	2	US-08-764-100-25	Sequence 25, Appl
343	32	42.7	772	2	US-09-252-991A-30121	Sequence 30121, A
344	32	42.7	783	2	US-09-252-991A-18035	Sequence 18035, A
345	32	42.7	805	2	US-10-158-847-142	Sequence 142, App
346	32	42.7	805	2	US-10-158-825-142	Sequence 142, App
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355	32	42.7	890	2	US-09-252-991A-19574	Sequence 19574, A
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358	32	42.7	924	2	US-09-270-767-46470	Sequence 46470, A
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907	30	40.0	1581	2	US-09-110-517-2	Sequence 2, Appli
908	30	40.0	1770	2	US-09-487-558B-298	Sequence 298, App
909	30	40.0	1956	2	US-09-843-417-10	Sequence 10, Appl
910	30	40.0	1956	2	US-09-527-013-10	Sequence 10, Appl
911	30	40.0	2221	2	US-08-815-927-27	Sequence 27, Appl
912	30	40.0	2221	2	US-09-144-198-30	Sequence 30, Appl
913	30	40.0	3290	2	US-09-328-352-5496	Sequence 5496, Ap
914	30	40.0	4019	2	US-09-854-133-425	Sequence 425, App
915	30	40.0	5588	2	US-09-036-987A-6	Sequence 6, Appli
916	30	40.0	5588	2	US-09-370-700-6	Sequence 6, Appli
917	30	40.0	5588	2	US-09-603-207-6	Sequence 6, Appli
918	29.5	39.3	91	2	US-09-270-767-33969	Sequence 33969, A
919	29.5	39.3	148	2	US-09-916-510A-3	Sequence 3, Appli
920	29.5	39.3	205	1	US-09-107-532A-5214	Sequence 5214, Ap
921	29.5	39.3	227	2	US-08-164-292B-27	Sequence 27, Appl
922	29.5	39.3	227	2	US-09-845-622-27	Sequence 27, Appl
923	29.5	39.3	227	2	US-09-815-927-27	Sequence 27, Appl
924	29.5	39.3	227	4	US-09-103-330-27	Sequence 27, Appl
925	29.5	39.3	227	2	US-09-435-244-27	Sequence 27, Appl
926	29.5	39.3	243	2	US-09-767-465571	Sequence 46571, A
927	29.5	39.3	287	2	US-09-767-45754	Sequence 45754, A
928	29.5	39.3	306	2	US-08-980-832-40	Sequence 40, Appl
929	29.5	39.3	391	2	US-09-920-923B-40	Sequence 40, Appl
930	29.5	39.3	391	2	US-09-326-529-2	Sequence 2, Appli
931	29.5	39.3	478	2	US-09-326-529-4	Sequence 4, Appli
932	29.5	39.3	478	4	US-09-703-809A-2	Sequence 2, Appli
933	29.5	39.3	678	2	US-09-120-663-2	Sequence 2, Appli
934	29.5	39.3	802	1	US-09-431-614-8	Sequence 8, Appli
935	29.5	39.3	802	2	US-09-596-784-2	Sequence 2, Appli
936	29.5	39.3	802	1	US-08-326-286-4	Sequence 4, Appli
937	29.5	39.3	1181	2	US-08-471-052A-83	Sequence 83, Appl
938	29.5	39.3	1182	1	US-08-189-331-83	Sequence 83, Appl
939	29.5	39.3	1838	2	US-09-120-529-4	Sequence 4, Appli
940	29.5	39.3	1838	1	US-08-471-800-83	Sequence 83, Appl
941	29.5	39.3	1838	2	US-08-471-068-83	Sequence 83, Appl
942	29.3	39.3	1838	2	US-09-412-100-28	Sequence 28, Appl
943	29	38.7	33	2	US-09-177-294-42	Sequence 42, Appl
944	29	38.7	38	2	US-09-812-283-42	Sequence 42, Appl
945	29	38.7	38	1	US-08-176-500-83	Sequence 83, Appl
946	29	38.7	44	2	US-08-471-052A-83	Sequence 83, Appl
947	29	38.7	44	2	US-09-099-639-16	Sequence 16, Appl
948	29	38.7	44	4	US-08-471-939-83	Sequence 83, Appl
949	29	38.7	44	1	US-08-471-800-83	Sequence 83, Appl
950	29	38.7	38	1	US-08-906-397A-16	Sequence 16, Appl
951	29	38.7	44	1	US-08-471-068-83	Sequence 83, Appl
952	29	38.7	44	2	US-08-453-274B-16	Sequence 16, Appl
953	29	38.7	44	1	US-08-453-699A-16	Sequence 16, Appl
954	29	38.7	44	2	US-08-268-161A-16	Sequence 16, Appl
955	29	38.7	44	2	US-08-453-702A-16	Sequence 16, Appl
956	29	38.7	44	2	US-09-162-934-11	Sequence 11, Appl
957	29	38.7	44	4	PCT-US95-08071-16	Sequence 16, Appl
958	29	38.7	44	2	US-09-812-528-11	Sequence 11, Appl
959	29	38.7	60	2	US-08-466-033-241	Sequence 241, App
960	29	38.7	60	2	US-08-461-134-241	Sequence 241, App
961	29	38.7	61	2	US-08-464-733-241	Sequence 241, App
962	29	38.7	61	2	US-08-444-733-241	Sequence 241, App
963	29	38.7	61	1	US-08-461-361-241	Sequence 241, App
964	29	38.7	61	2	US-09-252-991A-24069	Sequence 24069, A
965	29	38.7	61	1	US-09-732-210-504	Sequence 504, App
966	29	38.7	65	2	US-09-485-910-241	Sequence 241, App
967	29	38.7	67	2	US-08-039-857-31	Sequence 31, Appl
968	29	38.7	70	2	US-08-691-641-15	Sequence 15, Appl
969	29	38.7	70	1	US-08-466-033-185	Sequence 185, App
970	29	38.7	70	1	US-08-444-773-185	Sequence 185, App
971	29	38.7	70	1	US-08-464-134-185	Sequence 185, App
972	29	38.7	70	1	US-08-461-361-185	Sequence 185, App
973	29	38.7	70	2	US-08-485-910-185	Sequence 185, App
974	29	38.7	73	2	US-09-248-796A-25924	Sequence 25924, A
975	29	38.7	77	2	US-09-511-999C-4965	Sequence 4965, Ap
976	29	38.7	80	1	US-08-487-001A-33	Sequence 33, Appl

977	29	38.7	80	1	US-08-630-822A-33	Sequence 33, Appl
978	29	38.7	80	1	US-09-005-069-33	Sequence 33, Appl
979	29	38.7	91	2	US-09-270-767-34371	Sequence 34371, A
980	29	38.7	91	2	US-09-270-767-49588	Sequence 49588, A
981	29	38.7	92	2	US-09-270-767-47252	Sequence 47252, A
982	29	38.7	92	2	US-09-513-999C-6834	Sequence 6834, Ap
983	29	38.7	97	2	US-09-107-532A-3871	Sequence 3871, Ap
984	29	38.7	100	2	US-09-732-210-1165	Sequence 1165, Ap
985	29	38.7	104	2	US-09-270-767-34112	Sequence 34112, A
986	29	38.7	104	2	US-09-270-767-49329	Sequence 49329, A
987	29	38.7	104	2	US-09-248-796A-16122	Sequence 16122, A
988	29	38.7	105	2	US-09-252-991A-27753	Sequence 27753, A
989	29	38.7	105	2	US-09-248-796A-18467	Sequence 18467, A
990	29	38.7	106	2	US-09-513-999C-7677	Sequence 7677, Ap
991	29	38.7	106	2	US-09-513-999C-9415	Sequence 9415, Ap
992	29	38.7	116	2	US-09-489-039A-9434	Sequence 9434, Ap
993	29	38.7	120	2	US-09-902-540-13733	Sequence 13733, A
994	29	38.7	128	2	US-09-513-999C-8112	Sequence 8112, Ap
995	29	38.7	131	1	US-08-466-033C-179	Sequence 179, App
996	29	38.7	131	1	US-09-444-733-179	Sequence 179, App
997	29	38.7	131	1	US-08-464-134-179	Sequence 179, App
998	29	38.7	131	1	US-08-461-361-179	Sequence 179, App
999	29	38.7	131	1	US-08-485-910-179	Sequence 179, App
1000	29	38.7	131	2	US-09-489-039A-10730	Sequence 10730, A

ALIGNMENTS

RESULT 1
US-09-209-916-1
; Sequence 1, Application US/09209916
; Patent No. 638703
; GENERAL INFORMATION:
; APPLICANT: Cho, Myung-Sam
; APPLICANT: Chan, Sham-Yuen
; APPLICANT: Kelsey, William
; APPLICANT: Yee, Helena
; TITLE OF INVENTION: Expression System for Factor VIII
; FILE REFERENCE: MSB-7255
; CURRENT APPLICATION NUMBER: US/09/209,916
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 1
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Derived from
; OTHER INFORMATION: human factor VIII sequence
US-09-209-916-1

Query Match   100.0%; Score 75; DB 2; Length 1438;
Best Local Similarity   100.0%; Pred. No. 5.4e-05;
Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MSSSPHVLRNRAQSG 15
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Db   817 MSSSPHVLRNRAQSG 831

RESULT 2
US-09-407-605-3
; Sequence 3, Application US/0940760S
; Patent No. 6924365
; GENERAL INFORMATION:
; APPLICANT: Selden, Richard F.
; APPLICANT: Miller, Allan M.
; APPLICANT: Treco, Douglas A.
; TITLE OF INVENTION: OPTIMIZED MESSENGER RNA
; FILE REFERENCE: 10278-009001
; CURRENT APPLICATION NUMBER: US/09/407,605
; CURRENT FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/130,241
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: 60/102,239
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 3
; LENGTH: 1445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated peptide
US-09-407-605-3

Query Match   100.0%; Score 75; DB 2; Length 1445;
Best Local Similarity   100.0%; Pred. No. 5.5e-05;
Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MSSSPHVLRNRAQSG 15
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Db   824 MSSSPHVLRNRAQSG 838

RESULT 3
US-09-407-605-4
; Sequence 4, Application US/0940760S
; Patent No. 6924365
; GENERAL INFORMATION:
; APPLICANT: Selden, Richard F.
; APPLICANT: Miller, Allan M.
; APPLICANT: Treco, Douglas A.
; TITLE OF INVENTION: OPTIMIZED MESSENGER RNA
; FILE REFERENCE: 10278-009001
; CURRENT APPLICATION NUMBER: US/09/407,605
; CURRENT FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/130,241
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: 60/102,239
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 4
; LENGTH: 1447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated peptide
US-09-407-605-4

Query Match   100.0%; Score 75; DB 2; Length 1447;
Best Local Similarity   100.0%; Pred. No. 5.5e-05;
Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MSSSPHVLRNRAQSG 15
              |||||||||||||||
Db   826 MSSSPHVLRNRAQSG 840

RESULT 4
US-09-001-039B-47
; Sequence 47, Application US/0900109B
; Patent No. 6818439
; GENERAL INFORMATION:
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Respess, James G.
; APPLICANT: DePolo, Nicholas J.
; APPLICANT: Hsu, David Chi-Tang
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Greengard, Judith
; APPLICANT: Lee, Will
; TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF

OM protein - protein search, using sw model

GenCore version 5.1.6

Run on: November 25, 2005, 22:59:08 ; Search time 37.3448 Seconds
(without alignments)
283.384 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
Sequence: 1 MSSSPHVLRNRAQSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	DB ID	Description
1	75	100.0	2351	1	FA8_HUMAN	p00451	h coagulati
2	75	100.0	2351	1	Q5HY69_HUMAN	q5hy69	homo sapien
3	69	92.0	2343	1	FA8_CANFA	o18806	canis famil
4	56	74.7	2133	1	FA8_PIG	p12263	sus scrofa
5	50	66.7	313	2	Q5DBY4_SCHJA	q5dby4	schistosoma
6	50	66.7	440	2	Q9KLN7_VIBCH	q9kln7	vibrio chol
7	49	65.3	288	2	Q5LLG7_SILPO	q5llg7	silicibacte
8	46	61.3	332	2	Q5SR49_CRYNE	q5sr49	cryptococcu
9	46	61.3	355	2	Q5KF20_CRYNE	q5kf20	cryptococcu
10	43	57.3	282	2	Q63Y07_BURPS	q63y07	burkholderi
11	43	57.3	282	2	Q62MY6_BURMA	q62my6	burkholderi
12	43	57.3	290	2	Q7VZE1_BORPE	q7vze1	bordetella
13	43	57.3	290	2	Q7WGW7_BORBR	q7wgw7	bordetella
14	43	57.3	2319	1	FA8_MOUSE	q06194	mus musculu
15	42	56.0	206	2	Q5Z752_ORYSA	q5z752	oryza sativ
16	42	56.0	355	1	P36992	p36992	pleuronecte
17	42	56.0	827	2	Q4R3D7_MACFA	q4r3d7	macaca fasc
18	41	54.7	349	2	Q8D3B4_WIGBR	q8d3b4	wiggleswort
19	41	54.7	772	2	Q529F6_MAGGR	q529f6	magnaporthe
20	41	54.7	1155	2	Q54NV0_DICDI	q54nv0	dictyosteli
21	41	54.7	1846	2	Q4W073_ASPFU	q4w073	aspergillus
22	40	53.3	69	2	Q6K254_ORYSA	q6k254	oryza sativ
23	40	53.3	133	2	Q92490_9BACI	q92490	bacillus sp
24	40	53.3	160	1	RUVX_GLUOX	q5fnd1	gluconobact
25	40	53.3	166	2	Q1GV6_DROME	q1gv6	drosophila
26	40	53.3	356	2	O86865_STRGA	o86865	streptomyce
27	40	53.3	390	2	Q9HYK3_PSEAE	q9hyk3	pseudomonas
28	40	53.3	439	2	Q820M8_NITEU	q820m8	nitrosomona
29	40	53.3	462	2	Q4LJ36_BURK	q4lj36	burkholderi
30	40	53.3	472	2	Q5ZR27_CAEEL	q5zr27	caenorhabdi
31	40	53.3	584	2	Q2ZZ92_RHIME	q2zz92	rhizobium m
32	40	53.3	621	1	DCTB_RHIME	p13633	rhizobium m
33	40	53.3	642	2	Q4X1O4_ASPFU	q4x1o4	aspergillus
34	40	53.3	711	2	Q6D6D1_ERWCT	q6d6d1	erwinia car
35	40	53.3	863	2	Q73D59_BACC1	q73d59	bacillus ce
36	39	52.0	1241	2	Q57WH0_9TRYP	q57wh0	trypanosoma
37	39	52.7	2473	1	Q46SB2_TETNG	q46sb2	tetraodon n
38	39	52.0	915	2	Q41P88_USTMA	q41p88	ustilago ma
39	39	52.0	88	2	Q9SL17_ARATH	q9sl17	arabidopsis
40	39	52.0	141	2	Q62SC7_ORYSA	q62sc7	oryza sativ
41	39	52.0	208	2	Q6FT33_CANGA	q6ft33	candida gla
42	39	52.0	297	2	Q72TM1_LEPIC	q72tm1	leptospira
43	39	52.0	312	2	Q8F1M8_LEPIN	q8f1m8	leptospira
44	39	52.0	297	1	XERC_CHLPN	q29f7	chlamydia p
45	39	52.0	349	2	Q51Y78_MAGGR	q51y78	magnaporthe
46	39	52.0	338	2	O8EE78_SHEON	o8ee78	shewanella
47	39	52.0	361	2	Q51K2_CRYNE	q51k2	cryptococcu
48	39	52.0	361	2	Q5K841_CRYNE	q5k841	cryptococcu
49	39	52.0	367	2	O8GAY4_BURST	o8gay4	burkholderi
50	39	52.0	384	2	Q7BTG9_PSEST	q7btg9	pseudomonas
51	39	52.0	387	2	Q74B19_GEOSL	q74b19	geobacter s
52	39	52.0	398	2	Q6XJ66_9PROT	q6xj66	kinetoplast
53	39	52.0	398	2	Q84BW7_9GAMM	q84bw7	endosymbion
54	39	52.0	434	2	O8NDN8_HUMAN	o8ndn8	homo sapien
55	39	52.0	434	1	Q5R460_PONPY	q5r460	pongo pygma
56	39	52.0	443	2	O12887_HUMAN	o12887	homo sapien
57	39	52.0	443	2	O8NFU0_HUMAN	o8nfu0	homo sapien
58	39	52.0	473	2	Q5JR93_HUMAN	q5jr93	homo sapien
59	39	52.0	473	2	O8R8M8_THETN	o8r8m8	thermoanaer
60	39	52.0	474	2	Q4WMC1_ASPFU	q4wmc1	aspergillus
61	39	52.0	487	2	Q7UTD0_RHOBA	q7utd0	rhodopirell
62	39	52.0	489	2	Q4FY15_LEIMA	q4fy15	leishmania
63	39	52.0	650	2	Q9H876_HUMAN	q9h876	homo sapien
64	39	52.0	744	2	Q9UJR6_SCHMA	q9ujr6	schistosoma
65	39	52.0	784	2	Q9YJJ4_SCHMA	q9yjj4	schistosoma
66	39	52.0	784	2	Q5LJP1_DROME	q5ljp1	drosophila
67	39	52.0	918	2	Q4RXM9_TETNG	q4rxm9	tetraodon n
68	39	52.0	982	2	Q5ITJ8_MAGGR	q5itj8	magnaporthe
69	39	52.0	1078	2	Q9F3J4_STRCO	q9f3j4	streptomyce
70	39	52.0	1096	2	Q6FVJ1_CANGA	q6fvj1	candida gla
71	39	52.0	1336	2	Q9H4G2_HUMAN	q9h4g2	homo sapien
72	39	52.0	1493	2	Q9ULL8_HUMAN	q9ull8	homo sapien
73	39	51.3	1502	2	Q80G66_HUMAN	q80g66	homo sapien
74	38.5	51.3	185	2	Q9X5S2_STRLA	q9x5s2	streptomyce
75	38.5	51.3	611	2	Q8TXL6_METKA	q8tx16	methanopyru
76	38	50.7	73	2	O86332_MYCTU	o86332	mycobacteri
77	38	50.7	101	2	Q7U194_MYCBO	q7u194	mycobacteri
78	38	50.7	101	2	O8N4Y0_HUMAN	o8n4y0	homo sapien
79	38	50.7	128	2	Q4LH64_9BURK	q4lh64	burkholderi
80	38	50.7	157	1	P72803_SYNY3	p72803	synechocyst
81	38	50.7	174	1	P38316_YEAST	p38316	saccharomyc
82	38	50.7	186	2	Q5RJS0_RAT	q5rj80	rattus norv
83	38	50.7	197	1	Q91XT1_RAT	q91xt1	rattus norv
84	38	50.7	250	2	Q90572_GINCI	q90572	ginglymosto
85	38	50.7	259	2	Q7K405_TRICA	q7k405	tribolium c
86	38	50.7	297	2	Q9ATD5_GOSHI	q9atd5	goshiya h
87	38	50.7	302	1	Q9FDG0_BRUAB	q9fdg0	brucella ab
88	38	50.7	309	2	Q9AWM1_ORYSA	q9awm1	oryza sativ
89	38	50.7	324	2	Q9F5Q1_ECTVA	q9f5q1	ectovA
90	38	50.7	351	2	Q8KTR5_CANTP	q8ktr5	candidatus
91	38	50.7	351	1	AROC_MANSM	q92b53	mannheimia
92	38	50.7	359	2	Q4LSU3_9BURK	q4lsu3	burkholderi
93	38	50.7	367	1	Q41SU3_9BURK	q41su3	alcaligenes
94	38	50.7	390	2	Q9ZB53_9BURK	q9zb53	burkholderi
95	38	50.7	392	2	Q9NDB6_RHOPA	q9ndb6	ectothiorho
96	38	50.7	394	2	Q86BF2_DROME	q86bf2	rhodopseudo
97	38	50.7	394	2	Q41757_MAIZE	q41757	drosophila
98	38	50.7	399	2	Q6F2D9_SOLDE	q6f2d9	zea mays (m
99	38	50.7	399	2	Q87LD6_VIBPA	q87ld6	solanum dem
100	38	50.7	405	2	Q7NG50_GLOVI	q7ng50	drosophila
101	38	50.7	405	2	Q5HZ82_XENLA	q5hz82	gloeobacter
102	38	50.7	445	2	Q9SKG0_ARATH	q9skg0	vibrio para
103	38	50.7	447	2	O70653_GALV	o70653	xenopus lae
104	38	50.7	473	2	Q9YWM0_GALV	q9ywm0	arabidopsis

No	%1	%2	Len	n	Accession	id	Organism
105	38	50.7	752	2	Q4WKC8_ASPFU	q4wkc8	aspergillus
106	38	50.7	785	2	Q8BNG6_MOUSE	q8bng6	mus musculu
107	38	50.7	846	2	Q584Y3_9TRYP	q584y3	trypanosoma
108	38	50.7	851	2	Q4WE57_ASPFU	q4we57	aspergillus
109	38	50.7	935	2	Q5U4H2_MOUSE	q5u4h2	mus musculu
110	38	50.7	1089	2	Q7Q135_ANOGA	q7q135	anopheles g
111	38	50.7	1473	2	Q54TV0_DICDI	q54tv0	dictyosteli
112	38	50.7	1589	2	Q6GQV9_MOUSE	q6gqv9	mus musculu
113	38	50.7	2204	2	Q7T7P5_9ENTO	q7t7p5	human coxsa
114	38	50.7	2381	2	Q5TNW9_ANOGA	q5tnw9	anopheles g
115	38	50.7	2414	1	Q09472_HUMAN	q09472	homo sapien
116	38	50.7	2414	2	Q5W1B6_HUMAN	q5w1b6	homo sapien
117	38	50.7	2429	2	Q8QZV8_MOUSE	q8qzv8	mus musculu
118	38	50.7	2441	1	CBP_MOUSE	P45481	mus musculu
119	38	50.7	2442	2	Q6JHU9_RAT	q6jhu9	rattus norv
120	38	50.7	131	2	Q5C662_SCHJA	q5c662	schistosoma
121	37.5	50.0	131	2	Q8ZM97_SALTY	q8zm97	salmonella
122	37.5	50.0	392	2	Q5FEP2_SALPA	q5fep2	salmonella
123	37.5	50.0	392	2	Q5HJD3_STAAC	q5hjd3	staphylococ
124	37.5	50.0	698	2	Q7A7W0_STAAN	q7a7w0	staphylococ
125	37.5	50.0	698	2	Q8NYI2_STAAM	q8nyi2	staphylococ
126	37.5	50.0	698	2	Q99WX9_STAAM	q99wx9	staphylococ
127	37.5	50.0	705	2	Q6GCN0_STAAS	q6gcn0	staphylococ
128	38	49.3	76	2	Q4KB77_PSEF5	q4kb77	pseudomonas
129	38	49.3	133	2	Q9M9Q8_ARATH	q9m9q8	arabidopsis
130	38	49.3	138	2	O05549_LISMO	o05549	listeria mo
131	38	49.3	140	2	Q95SC6_DROME	q95sc6	drosophila
132	38	49.3	161	2	Q5KG97_CRYNE	q5kg97	cryptococcu
133	38	49.3	161	2	Q5K941_CRYNE	q5k941	cryptococcu
134	38	49.3	187	2	Q63KK1_BURPS	q63kk1	burkholderi
135	38	49.3	200	2	P95471_PSEFL	p95471	pseudomonas
136	38	49.3	217	2	Q62CI4_BURMA	q62ci4	burkholderi
137	38	49.3	217	2	Q7XJ03_ORYSA	q7xj03	oryza sativ
138	38	49.3	227	2	Q7MU67_PORGI	q7mu67	porphyromon
139	38	49.3	227	2	Q4ZP22_PSESY	q4zp22	pseudomonas
140	38	49.3	227	2	Q93SN1_PSEPU	q93sn1	pseudomonas
141	38	49.3	227	2	Q4K766_PSEF5	q4k766	pseudomonas
142	38	49.3	227	2	Q87XI6_PSESM	q87xi6	pseudomonas
143	38	49.3	227	2	Q88PE9_PSEPK	q88pe9	pseudomonas
144	38	49.3	234	2	Q8MKV1_DROME	q8mkv1	drosophila
145	38	49.3	236	2	Q416K4_GIBZE	q416k4	gibberella
146	38	49.3	245	2	P91668_DROME	p91668	drosophila
147	38	49.3	245	2	Q94536_DROME	q94536	drosophila
148	38	49.3	259	2	Q8GSH4_BIFLO	q8gsh4	bifidobacte
149	38	49.3	271	2	Q50EC6_STRFL	q50ec6	streptomyce
150	38	49.3	279	2	Q4NHT8_9MICC	q4nht8	arthrobacte
151	38	49.3	282	2	Q93ME7_AMYMD	q93me7	amycolatops
152	38	49.3	283	2	Q5IE14_BACFN	q5ie14	bacteroides
153	38	49.3	283	2	Q64V51_BACFR	q64v51	bacteroides
154	38	49.3	318	2	Q6BFX6_PARTE	q6bfx6	paramecium
155	38	49.3	338	2	Q4HVX9_GIBZE	q4hvx9	gibberella
156	38	49.3	360	2	Q62D41_YERPE	q62d41	yersinia pe
157	38	49.3	361	1	Q5F2M6_YERPS	q5f2m6	yersinia ps
158	38	49.3	361	1	O668V5_YERPS	o668v5	yersinia ps
159	38	49.3	366	1	Q7NYT5_CHRVO	q7nyt5	chromobacte
160	38	49.3	366	1	Q8X240_RALSO	q8x240	ralstonia s
161	38	49.3	366	2	Q4LIQ3_9BURK	q4liq3	burkholderi
162	38	49.3	369	1	Q62KU7_9BURK	q62ku7	burkholderi
163	38	49.3	369	2	Q63TK6_9BURK	q63tk6	burkholderi
164	38	49.3	377	1	Q5P1K1_AZOSE	q5p1k1	azoarcus sp
165	38	49.3	381	2	Q6K307_ORYSA	q6k307	oryza sativ
166	38	49.3	383	2	Q6G9S9_STAAS	q6g9s9	staphylococ
167	38	49.3	383	2	Q6GHF1_STAAR	q6ghf1	staphylococ
168	38	49.3	383	2	Q5HGE7_STAAC	q5hge7	staphylococ
169	38	49.3	383	2	Q7A5W9_STAAN	q7a5w9	staphylococ
170	38	49.3	383	2	Q8NWY3_STAAM	q8nwy3	staphylococ
171	38	49.3	385	2	Q99UI8_STAAM	q99ui8	staphylococ
172	38	49.3	392	2	Q6KD06_ORYSA	q6kd06	oryza sativ
173	38	49.3	392	2	Q9ZGI9_9BURK	q9zgi9	alcaligenes
174	38	49.3	393	2	Q4LM20_9BURK	q4lm20	burkholderi
175	38	49.3	393	2	Q41PE9_9BURK	q41pe9	burkholderi
176	38	49.3	404	2	Q648M8_9ARCH	q648m8	uncultured
177	38	49.3	407	2	Q5BTP6_RHIME	q5btp6	rhizobium m
178	37	49.3	414	2	Q7SGE9_NEUCR	q7sge9	neurospora
179	37	49.3	423	2	Q67SG8_SYMTH	q67sg8	symbiobacte
180	37	49.3	426	2	Q4GZB6_9TRYP	q4gzb6	trypanosoma
181	37	49.3	443	1	COX10_MOUSE	cox10 mouse	mus musculu
182	37	49.3	447	2	Q8DE97_VIBVU	q8de97	vibrio vuln
183	37	49.3	447	2	Q7MPC3_VIBVY	q7mpc3	vibrio vuln
184	37	49.3	451	2	O35390_RAT	o35390	rattus norv
185	37	49.3	451	2	Q7GGI5_ANOGA	q7ggi5	anopheles g
186	37	49.3	467	2	Q7XBS1_ORYSA	q7xbs1	oryza sativ
187	37	49.3	475	2	Q9FRN5_ORYSA	q9frn5	oryza sativ
188	37	49.3	475	2	Q7Y2B4_BPR69	q7y2b4	bacteriopha
189	37	49.3	516	2	Q4HY00_GIBZE	q4hy00	gibberella
190	37	49.3	519	2	Q5GUD7_XANOR	q5gud7	xanthomonas
191	37	49.3	529	2	Q7LSZ7_HUMAN	q7lsz7	homo sapien
192	37	49.3	534	2	Q61CS6_CAEBR	q61cs6	caenorhabdi
193	37	49.3	548	2	Q8WU59_HUMAN	q8wu59	homo sapien
194	37	49.3	552	2	Q94DS2_ORYSA	q94ds2	oryza sativ
195	37	49.3	553	2	Q4QLZ7_LEIMA	q4qlz7	leishmania
196	37	49.3	561	2	Q52VR0_WHEAT	q52vr0	triticum ae
197	37	49.3	575	1	O19201_CAEEL	o19201	caenorhabdi
198	37	49.3	575	1	GAB2_HUMAN	gab2 human	homo sapien
199	37	49.3	591	1	Q5HJA7_XANOR	q5hja7	xanthomonas
200	37	49.3	595	2	Q612G8_CAEBR	q612g8	caenorhabdi
201	37	49.3	630	2	Q55MU6_CRYNE	q55mu6	cryptococcu
202	37	49.3	631	2	Q5KB73_CRYNE	q5kb73	cryptococcu
203	37	49.3	631	2	Q9N6I5_LEISM	q9n6i5	leishmania
204	37	49.3	637	2	GAB2_RAT	gab2 rat	rattus norv
205	37	49.3	638	1	Q7XWU2_ORYSA	q7xwu2	oryza sativ
206	37	49.3	647	1	Q61FL2_CAEBR	q61fl2	caenorhabdi
207	37	49.3	665	2	O19201_CAEEL	o19201	caenorhabdi
208	37	49.3	665	2	GAB2_HUMAN	gab2 human	homo sapien
209	37	49.3	666	2	Q92I88_METMA	q92i88	methanosarc
210	37	49.3	667	2	Q9EQH1_RAT	q9eqh1	rattus norv
211	37	49.3	676	1	GAB2_MOUSE	gab2 mouse	mus musculu
212	37	49.3	697	2	Q8PX77_METMA	q8px77	methanosarc
213	37	49.3	702	2	Q52ZW8_CRYNE	q52zw8	cryptococcu
214	37	49.3	732	2	Q8C8V4_MOUSE	q8c8v4	mus musculu
215	37	49.3	732	2	Q5JRW7_HUMAN	q5jrw7	homo sapien
216	37	49.3	738	2	Q5V8I1_BRARE	q5v8i1	brachydanio
217	37	49.3	744	2	Q85YR8_DROME	q85yr8	drosophila
218	37	49.3	853	2	Q9VZD7_DROME	q9vzd7	drosophila
219	37	49.3	854	2	Q9UPP8_HUMAN	q9upp8	homo sapien
220	37	49.3	875	2	Q4W8R3_HORVU	q4w8r3	hordeum vul
221	37	49.3	876	2	Q8BM5_HUMAN	q8bm5	homo sapien
222	37	49.3	886	2	Q9H8M5_HUMAN	q9h8m5	homo sapien
223	37	49.3	969	2	Q55S69_HUMAN	q55s69	homo sapien
224	37	49.3	981	2	Q5U2P1_RAT	q5u2p1	rattus norv
225	37	49.3	1022	2	Q5T570_HUMAN	q5t570	homo sapien
226	37	49.3	1037	2	Q9VM64_DROME	q9vm64	drosophila
227	37	49.3	1037	2	Q98TD0_CHICK	q98td0	gallus gall
228	37	49.3	1037	2	Q825B5_STRAW	q825b5	streptomyce
229	37	49.3	1038	2	Q63R8_TETNG	q63r8	tetraodon n
230	37	49.3	1052	2	Q9BS16_HUMAN	q9bs16	homo sapien
231	37	49.3	1059	2	Q5JRX3_HUMAN	q5jrx3	homo sapien
232	37	49.3	1061	2	Q4VBR1_HUMAN	q4vbr1	homo sapien
233	37	49.3	1074	2	Q4VBR1_HUMAN	q4vbr1	homo sapien
234	37	49.3	1106	2	Q9M297_ARATH	q9m297	arabidopsis
235	37	49.3	1256	2	Q5RDG3_PONPY	q5rdg3	pongo pygma
236	37	49.3	1395	2	Q95204_HUMAN	q95204	homo sapien
237	37	49.3	1437	2	O23424_ARATH	o23424	arabidopsis
238	37	49.3	1607	2	Q8GY51_ARATH	q8gy51	arabidopsis
239	37	49.3	1729	2	Q7U913_SYNPX	q7u913	synechococc
240	37	49.3	1744	2	Q4NED9_9DELT	q4ned9	anaeromyxob
241	37	49.3	1900	2	Q7SDF9_NEUCR	q7sdf9	neurospora
242	37	49.3	1999	2	Q4YAG7_PLABE	q4yag7	plasmodium
243	37	49.3	2072	2	Q4ABD0_TETNG	q4abd0	tetraodon n
244	37	49.3	2396	2	Q5U132_RHOBA	q5u132	rhodopirell
245	37	49.3	2713	2	Q7U132_RHOBA	q7u132	rhodopirell
246	36.5	48.7	393	2	Q6DLL1_ERWCT	q6dll1	erwinia car
247	36.5	48.7	394	1	YQEF_ECOLI	yqef ecoli	escherichia
248	36.5	48.7	394	2	Q8X617_ECO57	q8x617	escherichia
249	36.5	48.7	497	2	Q8F696_ECOLI	q8f696	escherichia
250	36.5	48.7	497	2	Q74KX5_THET2	q74kx5	thermus the

No.					ID	Description
251	36.5	48.7	497	2	Q53W69_THET8	thermus the
252	36.5	48.7	716	2	Q4Q3G1_LEIMA	leishmania
253	36.5	48.7	970	2	Q7RXP7_NEUCR	neurospora
254	36	48.7	62	2	Q41571_WHEAT	triticum ae
255	36	48.0	87	2	Q4TG48_TETNG	tetraodon n
256	36	48.0	96	2	Q88AT9_PSESM	pseudomonas
257	36	48.0	119	2	Q74A28_GEOSL	geobacter s
258	36	48.0	153	2	Q930P2_RHIME	rhizobium m
259	36	48.0	155	2	Q7UGT7_RHODA	rhodopirell
260	36	48.0	177	2	Q6USZ8_9SMEG	syngnathus
261	36	48.0	181	2	Q91TT4_TUHVI	tupaiid her
262	36	48.0	192	1	Y4LH_RHISN	rhizobium s
263	36	48.0	206	2	Q87CQ7_XYLFT	xylella fas
264	36	48.0	226	2	Q7P1Z6_DROME	drosophila
265	36	48.0	227	2	Q9HW21_PSEAE	pseudomonas
266	36	48.0	236	2	Q4YE08_PLABE	plasmodium
267	36	48.0	242	2	Q9KA99_BACHD	bacillus ha
268	36	48.0	244	2	Q8ELB2_OCEIH	oceanobacil
269	36	48.0	248	2	Q4H5F1_9DEIO	deinococcus
270	36	48.0	254	2	Q9KZD4_STRCO	streptomyce
271	36	48.0	268	2	Q9APU3_PSEAE	pseudomonas
272	36	48.0	276	2	Q7NU01_CHRVO	chromobacte
273	36	48.0	287	2	Q6CE60_YARLI	yarrowia li
274	36	48.0	297	2	Q9W2B4_DROME	drosophila
275	36	48.0	300	2	Q4THH6_TETNG	tetraodon n
276	36	48.0	312	2	Q5XXE2_PHACH	phanerochae
277	36	48.0	312	2	Q5I6G3_CHLAB	chlamydophi
278	36	48.0	312	2	Q823T9_CHLCV	chlamydophi
279	36	48.0	315	1	Q9PK47_CHLMU	chlamydia m
280	36	48.0	315	2	Q5XXE3_PHACH	phanerochae
281	36	48.0	315	2	Q5XXE5_PHACH	phanerochae
282	36	48.0	315	2	Q4NECO_9MICC	arthrobacte
283	36	48.0	319	2	Q5I8Y2_SILPO	silicibacte
284	36	48.0	331	2	Q9R6M3_9RHIZ	agrobacteri
285	36	48.0	333	2	Q8KGP6_RHILO	rhizobium l
286	36	48.0	338	1	6PGL_CANBF	candida
287	36	48.0	343	2	Q9SVJ6_ARATH	arabidopsis
288	36	48.0	344	1	Q9WDB1_9INFB	influenza b
289	36	48.0	353	1	AROC_BORBR	bordetella
290	36	48.0	353	1	AROC_BORPA	bordetella
291	36	48.0	353	1	AROC_BORPE	bordetella
292	36	48.0	356	2	Q8Y230_RALSO	ralstonia s
293	36	48.0	357	1	Q7VRU6_candidatus	candidatus
294	36	48.0	382	2	AROC_CANBF	candida
295	36	48.0	393	2	Q61J96_CAEBR	caenorhabdi
296	36	48.0	393	2	Q8F8U5_LEPIN	leptospira
297	36	48.0	393	2	Q72VA5_LEPIC	leptospira
298	36	48.0	395	2	Q6J504_BRARE	brachydanio
299	36	48.0	397	2	Q577S7_BRUAB	brucella ab
300	36	48.0	398	2	Q4K6J8_PSEF5	pseudomonas
301	36	48.0	398	2	Q5XEU6_ARATH	arabidopsis
302	36	48.0	407	2	Q6IVW0_BRARE	brachydanio
303	36	48.0	407	2	Q56HB0_BRARE	brachydanio
304	36	48.0	407	2	Q5O2T5_BRARE	brachydanio
305	36	48.0	409	2	Q4IZ68_AZOVI	azotobacter
306	36	48.0	410	2	Q8FWD1_BRUSU	brucella su
307	36	48.0	410	2	Q8YBY8_BRUME	brucella me
308	36	48.0	424	2	Q18207_CAEEL	caenorhabdi
309	36	48.0	430	2	Q4LPR5_9BURK	burkholderi
310	36	48.0	430	2	Q852K2_ORYSA	oryza sativ
311	36	48.0	434	2	Q6FJ25_CANGA	candida gla
312	36	48.0	440	2	Q9CI2_BRAJA	bradyrhizob
313	36	48.0	447	2	Q9KP44_VIBCH	vibrio chol
314	36	48.0	456	2	Q70IZ5_9STRA	botrydiopsi
315	36	48.0	460	2	Q5E7H3_VIBF1	vibrio fisc
316	36	48.0	468	2	Q98C98_RHILO	rhizobium l
317	36	48.0	469	2	Q8G604_BIFLO	bifidobacte
318	36	48.0	473	2	Q6SP39_ORYSA	oryza sativ
319	36	48.0	476	2	Q83632_TREPA	treponema p
320	36	48.0	479	2	Q72EF9_DESVH	desulfovibr
321	36	48.0	488	2	Q4PAF7_USTMA	ustilago ma
322	36	48.0	516	2	Q49MLO_TETNG	tetraodon n
323	36	48.0	524	2	Q6Q2H6_DROYA	drosophila
324	36	48.0	525	2	Q8L3T2_ORYSA	oryza sativ
325	36	48.0	533	2	Q4WM21_ASPFU	aspergillus
326	36	48.0	540	2	Q82SN0_NITEU	nitrosomona
327	36	48.0	549	2	Q41HV0_GIBZE	gibberella
328	36	48.0	550	2	Q743G4_MYCPA	mycobacteri
329	36	48.0	551	2	Q93H30_STRAW	streptomyce
330	36	48.0	568	2	Q4PAU2_USTMA	ustilago ma
331	36	48.0	578	2	Q55PF0_CRYNE	cryptococcu
332	36	48.0	578	2	Q89RH2_BRAJA	bradyrhizob
333	36	48.0	580	2	Q5KE08_CRYNE	cryptococcu
334	36	48.0	580	2	Q41HJ4_GIBZE	gibberella
335	36	48.0	582	2	Q57UIO_9TRYP	trypanosoma
336	36	48.0	585	1	Q5YQI5_NOCFA	nocardia fa
337	36	48.0	595	1	THIC_XANAC	xanthomonas
338	36	48.0	610	2	Q6CLD5_KLULA	kluyveromyc
339	36	48.0	625	1	Q52FY4_MAGGR	magnaporthe
340	36	48.0	648	2	Q4P7X4_USTMA	ustilago ma
341	36	48.0	659	2	P52453_HUMAN	human herpe
342	36	48.0	661	2	P52454_HUMAN	human herpe
343	36	48.0	662	1	U1.06_HHV6U	human herpe
344	36	48.0	662	1	U1.06_HHV6Z	human herpe
345	36	48.0	662	2	Q785M3_9BETA	human herpe
346	36	48.0	662	2	Q57138_9BETA	human herpe
347	36	48.0	687	2	Q4T0L7_TETNG	tetraodon n
348	36	48.0	687	2	Q5NPM4_ZYMMO	zymomonas m
349	36	48.0	717	2	Q5H4R6_XANOR	xanthomonas
350	36	48.0	727	2	Q7S415_NEUCR	neurospora
351	36	48.0	738	2	Q54L8_MAGGR	magnaporthe
352	36	48.0	739	2	Q4SAG9_TETNG	tetraodon n
353	36	48.0	755	2	Q747A4_GEOSL	geobacter s
354	36	48.0	763	2	Q19070_CAEEL	caenorhabdi
355	36	48.0	766	2	Q583Q4_9TRYP	trypanosoma
356	36	48.0	849	2	Q5AX08_EMENI	aspergillus
357	36	48.0	882	2	Q5AX08_EMENI	emeni
358	36	48.0	882	1	Q25342_LEIMA	leishmania
359	36	48.0	925	2	Q4Q3G5_9TRYP	trypanosoma
360	36	48.0	925	2	Q23463_CAEBR	caenorhabdi
361	36	48.0	974	2	Q61J94_CAEBR	caenorhabdi
362	36	48.0	975	2	Q1SVB8_DICDI	dictyosteli
363	36	48.0	1037	2	Q7SB63_NEUCR	neurospora
364	36	48.0	1083	2	Q7PFP4_ANOGA	anopheles g
365	36	48.0	1110	2	Q6FLT9_CANGA	candida gla
366	36	48.0	1144	2	P92199_CAEEL	caenorhabdi
367	36	48.0	1173	2	Q4RNS0_TETNG	tetraodon n
368	36	48.0	1196	2	Q6FSL9_CANGA	candida gla
369	36	48.0	1208	2	Q6F819_DROME	drosophila
370	36	48.0	1226	2	Q8T3K2_DROME	drosophila
371	36	48.0	1226	2	Q9VX92_DROME	drosophila
372	36	48.0	1284	2	Q9WJ35_9VIRU	9viru
373	36	48.0	1320	2	Q8JJX0_9VIRU	arabidopsis
374	36	48.0	1330	2	Q6BJ19_DEBHA	debaryomyce
375	36	48.0	1364	2	Q94HW7_ARATH	arabidopsis
376	36	48.0	1431	2	Q94HW2_ARATH	arabidopsis
377	36	48.0	1442	2	Q7SB87_NEUCR	neurospora
378	36	48.0	1456	2	Q9SXQ3_ARATH	arabidopsis
379	36	48.0	1456	2	Q2FT94_ARATH	arabidopsis
380	36	48.0	1460	2	Q5AGZ6_CANAL	canal
381	36	48.0	1466	2	Q5AGZ6_CANAL	candida alb
382	36	48.0	1466	2	Q9SXQ1_ARATH	arabidopsis
383	36	48.0	1475	2	Q9SXQ4_ARATH	arabidopsis
384	36	48.0	1475	2	Q6C6R0_YARLI	arabidopsis
385	36	48.0	1518	2	Q4RTT2_TETNG	trypanosoma
386	36	48.0	1600	2	Q4P2M4_USTMA	caenorhabdi
387	36	48.0	1647	2	Q4SVT8_TETNG	tetraodon n
388	36	48.0	1681	2	Q41KH0_GIBZE	drosophila
389	36	35.5	1774	2	Q93Y68_ORYSA	oryza sativ
390	36	35.5	1829	2	Q5WA9_9TRYP	trypanosoma
391	36	35.5	1845	2	Q4HV14_9TRYP	gibberella
392	36	35.5	2190	2	Q4HV14_9TRYP	trypanosoma
393	36	35.5	2503	2	Q57ZZ0_9TRYP	mus musculu
394	36	47.3	127	2	Q9DIU9_MOUSE	mus musculu
395	36	47.3	338	2	Q98LI1_RHILO	rhizobium l
396	36	47.3	392	2	Q87H42_VIBPA	vibrio para

No.	A	B	Len	N	Accession	Description
397	35.5	47.3	440	2	Q9KSD9_VIBCH	q9ksd9 vibrio chol
398	35.5	47.3	790	2	Q9SB53_ARATH	q9sb53 arabidopsis
399	35.5	47.3	1925	2	Q4Q1I0_LEIMA	q4q1i0 leishmania
400	35	46.7	65	2	Q8UZL0_9VIRU	q8uzl0 salmon panc
401	35	46.7	75	2	Q6SKF1_ARTAU	q6skf1 arthrobacte
402	35	46.7	79	2	Q8I602_PLAF7	q8i602 plasmodium
403	35	46.7	90	2	Q8CAG1_MOUSE	q8cag1 mus musculu
404	35	46.7	92	2	Q5RHY5_BRARE	q5rhy5 brachydanio
405	35	46.7	96	2	Q5Q0H9_ARATH	q5q0h9 arabidopsis
406	35	46.7	110	2	Q9HBX3_HUMAN	q9hbx3 homo sapien
407	35	46.7	115	2	Q6CP00_KLULA	q6cp00 kluyveromyc
408	35	46.7	128	2	Q5Q0I0_ARATH	q5q0i0 arabidopsis
409	35	46.7	131	2	Q8T540_PLAFA	q8t540 plasmodium
410	35	46.7	134	2	Q8T529_PLAFA	q8t529 plasmodium
411	35	46.7	137	2	Q9RT41_DEIRA	q9rt41 deinococcus
412	35	46.7	139	2	Q5BOJO_EMENI	q5bojo emericella
413	35	46.7	142	2	Q61IF2_MACRS	q61if2 macrobrachi
414	35	46.7	145	2	Q53QY2_HUMAN	q53qy2 homo sapien
415	35	46.7	156	2	Q4UTR5_XANCP	q4utr5 xanthomonas
416	35	46.7	162	1	RECX_XANCP	recx_xancp xanthomonas
417	35	46.7	162	2	Q6KAN5_MOUSE	q6kan5 mus musculu
418	35	46.7	163	2	Q6AN69_DESPS	q6an69 desulfotale
419	35	46.7	169	2	Q7D3T2_AGRT5	q7d3t2 agrobacteri
420	35	46.7	174	1	P20862 FANH_ECOLI	p20862 escherichia
421	35	46.7	175	2	Q4H506_DEIRA	q4h506 deinococcus
422	35	46.7	176	2	Q4H506_DEIRA	q4h506 deinococcus
423	35	46.7	178	2	Q97SY3_STRPN	q97sy3 streptococc
424	35	46.7	182	2	Q9FRC0_ORYSA	q9frc0 oryza sativ
425	35	46.7	187	2	Q8CWV9_STRR6	q8cwv9 streptococc
426	35	46.7	188	2	Q5AAW4_CANAL	q5aaw4 candida alb
427	35	46.7	191	2	Q5YFM5_9VIRU	q5yfm5 singapore g
428	35	46.7	194	2	Q8MV87_9TURB	q8mv87 thysanozoon
429	35	46.7	200	2	Q50DF6_9INFB	q50df6 influenza b
430	35	46.7	200	2	Q8MV92_DUGTI	q8mv92 dugesia tig
431	35	46.7	203	2	Q8MV88_9TURB	q8mv88 discocoelis
432	35	46.7	204	2	Q50DH4_9INFB	q50dh4 influenza b
433	35	46.7	204	2	Q4FQV1_9GAMM	q4fqv1 psychrobact
434	35	46.7	206	2	Q50DD1_9INFB	q50dd1 influenza b
435	35	46.7	208	2	Q50DF9_9INFB	q50df9 influenza b
436	35	46.7	211	2	Q50DG7_9INFB	q50dg7 influenza b
437	35	46.7	211	2	Q50DD0_9INFB	q50dd0 influenza b
438	35	46.7	212	2	Q50DD3_9INFB	q50dd3 influenza b
439	35	46.7	212	2	Q50DD4_9INFB	q50dd4 influenza b
440	35	46.7	212	2	Q50DD6_9INFB	q50dd6 influenza b
441	35	46.7	212	2	Q50DD7_9INFB	q50dd7 influenza b
442	35	46.7	212	2	Q50DF8_9INFB	q50df8 influenza b
443	35	46.7	212	2	Q50DG9_9INFB	q50dg9 influenza b
444	35	46.7	213	2	Q50DE7_9INFB	q50de7 influenza b
445	35	46.7	213	2	Q50DE0_9INFB	q50de0 influenza b
446	35	46.7	213	2	Q50DG1_9INFB	q50dg1 influenza b
447	35	46.7	214	2	Q50DE3_9INFB	q50de3 influenza b
448	35	46.7	214	2	Q50DG4_9INFB	q50dg4 influenza b
449	35	46.7	214	2	Q6MA61_PARUW	q6ma61 parachlamyd
450	35	46.7	217	2	Q50DH6_9INFB	q50dh6 influenza b
451	35	46.7	217	2	Q50DF5_9INFB	q50df5 influenza b
452	35	46.7	217	2	Q50DB5_9INFB	q50db5 influenza b
453	35	46.7	217	2	Q50DB4_9INFB	q50db4 influenza b
454	35	46.7	217	2	Q50DE4_9INFB	q50de4 influenza b
455	35	46.7	219	2	Q50DF7_9INFB	q50df7 influenza b
456	35	46.7	219	2	Q50DH0_9INFB	q50dh0 influenza b
457	35	46.7	221	2	Q91CN5_9INFB	q91cn5 influenza b
458	35	46.7	221	2	Q9WZX2_THEMA	q9wzx2 thermotoga
459	35	46.7	222	2	Q6U8H9_9INFB	q6u8h9 influenza b
460	35	46.7	222	2	Q98A52_RHILO	q98a52 rhizobium l
461	35	46.7	223	1	Q5HZW9_RAT	q5hzw9 rattus norv
462	35	46.7	223	2	P2O934_MOUSE	p2o934 mus musculu
463	35	46.7	223	2	Q6DKP1_MOUSE	q6dkp1 m ecotropic
464	35	46.7	226	2	Q50DH7_9INFB	q50dh7 influenza b
465	35	46.7	226	2	Q61EF9_CAEBR	q61ef9 caenorhabdi
466	35	46.7	227	2	Q61790_CAEBR	q61790 caenorhabdi
467	35	46.7	227	2	Q9ANC3_BRAJA	q9anc3 bradyrhizob
468	35	46.7	228	2	Q75T72_9INFB	q75t72 influenza b
469	35	46.7	230	2	Q53P18_ORYSA	q53p18 oryza sativ
467	35	46.7	231	2	Q53P18_ORYSA	q75t72 influenza b
468	35	46.7	231	2	Q75T72_9INFB	q53p18 oryza sativ
469	35	46.7	233	2	Q42ON3_PLABE	q42on3 plasmodium

No.	A	B	Len	N	Accession	Description
470	35	46.7	236	2	Q4LQZ4_9BURK	q4lqz4 burkholderi
471	35	46.7	236	2	Q8BG03_PSEPK	q8bg03 pseudomonas
472	35	46.7	238	2	Q226O0_CAEEL	q226o0 caenorhabdi
473	35	46.7	240	2	Q91CP9_9INFB	q91cp9 influenza b
474	35	46.7	240	2	Q50DE1_9INFB	q50de1 influenza b
475	35	46.7	240	2	Q50DE2_9INFB	q50de2 influenza b
476	35	46.7	242	2	Q50D81_9INFB	q50d81 influenza b
477	35	46.7	242	2	Q50DD5_9INFB	q50dd5 influenza b
478	35	46.7	243	2	Q50DD8_9INFB	q50dd8 influenza b
479	35	46.7	243	2	Q6U8I2_9INFB	q6u8i2 influenza b
480	35	46.7	243	2	Q91CQ0_9INFB	q91cq0 influenza b
481	35	46.7	245	2	Q50DA7_9INFB	q50da7 influenza b
482	35	46.7	246	2	Q6U8F6_9INFB	q6u8f6 influenza b
483	35	46.7	246	2	Q6U8E7_9INFB	q6u8e7 influenza b
484	35	46.7	257	2	Q6U8I5_9INFB	q6u8i5 influenza b
485	35	46.7	262	2	Q75T73_STAEP	q75t73 staphylococ
486	35	46.7	266	2	Q8CPF5_CORGL	q8cpf5 corynebacte
487	35	46.7	267	1	P55400 TRBJ_RHISN	p55400 rhizobium d
488	35	46.7	283	1	Q6MBC9_PARUW	q6mbc9 parachlamyd
489	35	46.7	289	2	Q4T6X8_TETNG	q4t6x8 tetraodon n
490	35	46.7	291	2	Q6I9X3_ORYSA	q6i9x3 oryza sativ
491	35	46.7	292	2	Q4RZES_TETNG	q4rzes tetraodon n
492	35	46.7	295	2	Q9HAD3_HUMAN	q9had3 homo sapien
493	35	46.7	295	2	Q4QIL4_LEIMA	q4qil4 leishmania
494	35	46.7	297	1	Q5SCC1_OSTTA	q5scc1 ostreococcu
495	35	46.7	297	1	Q2CPF0_PASMU	q2cpf0 pasteurella
496	35	46.7	298	2	Q65UK7_MANSM	q65uk7 mannheimia
497	35	46.7	298	2	Q5ZG64_9INFB	q5zg64 influenza b
498	35	46.7	298	2	Q4LCR3_9INFB	q4lcr3 influenza b
499	35	46.7	299	2	Q98K27_RHILO	q98k27 rhizobium 1
500	35	46.7	300	1	P59818 XERC_MYXXA	p59818 myxococcus
501	35	46.7	306	2	Q7V592_PROMM	q7v592 prochloroco
502	35	46.7	308	1	Q8JP44_9INFB	q8jp44 influenza b
503	35	46.7	309	1	Q8YJP2 XERD_BRUME	q8yjp2 brucella ne
504	35	46.7	309	1	Q72AN6 XERD_BRUSU	q72an6 brucella su
505	35	46.7	311	1	Q4LCS2_YARLI	q4lcs2 yarrowia li
506	35	46.7	317	2	Q6CAB9_YARLI	q6cab9 yarrowia li
507	35	46.7	318	2	Q80IY7_9INFB	q80iy7 influenza b
508	35	46.7	318	2	Q80IY8_9INFB	q80iy8 influenza b
509	35	46.7	318	2	Q80IY9_9INFB	q80iy9 influenza b
510	35	46.7	318	2	Q80IZ0_9INFB	q80iz0 influenza b
511	35	46.7	318	2	Q80IZ1_9INFB	q80iz1 influenza b
512	35	46.7	318	2	Q80IZ3_9INFB	q80iz3 influenza b
513	35	46.7	318	2	Q80IZ4_9INFB	q80iz4 influenza b
514	35	46.7	318	2	Q80IZ5_9INFB	q80iz5 influenza b
515	35	46.7	318	2	Q80IZ6_9INFB	q80iz6 influenza b
516	35	46.7	318	2	Q80IZ7_9INFB	q80iz7 influenza b
517	35	46.7	318	2	Q80IZ8_9INFB	q80iz8 influenza b
518	35	46.7	318	2	Q80IZ9_9INFB	q80iz9 influenza b
519	35	46.7	318	2	Q80J00_9INFB	q80j00 influenza b
520	35	46.7	318	2	Q80J01_9INFB	q80j01 influenza b
521	35	46.7	318	2	Q80J02_9INFB	q80j02 influenza b
522	35	46.7	318	2	Q80J04_9INFB	q80j04 influenza b
523	35	46.7	318	2	Q80J05_9INFB	q80j05 influenza b
524	35	46.7	318	2	Q80J06_9INFB	q80j06 influenza b
525	35	46.7	318	2	Q80J07_9INFB	q80j07 influenza b
526	35	46.7	318	2	Q80J08_9INFB	q80j08 influenza b
527	35	46.7	318	2	Q80J09_9INFB	q80j09 influenza b
528	35	46.7	318	2	Q80J10_9INFB	q80j10 influenza b
529	35	46.7	318	2	Q80J11_9INFB	q80j11 influenza b
530	35	46.7	318	2	Q80QY4_9INFB	q80qy4 influenza b
531	35	46.7	318	2	Q8BVC8_MOUSE	q8bvc8 mus musculu
532	35	46.7	321	2	Q5ZG67_9INFB	q5zg67 influenza b
533	35	46.7	322	2	Q6UUF4_ORYSA	q6uuf4 oryza sativ
534	35	46.7	323	2	Q5G967_9INFB	q5g967 influenza b
535	35	46.7	325	2	Q8JP55_9INFB	q8jp55 influenza b
536	35	46.7	326	2	Q8BAC7_9INFB	q8bac7 influenza b
537	35	46.7	326	2	Q8BAC8_9INFB	q8bac8 influenza b
538	35	46.7	326	2	Q8BAC9_9INFB	q8bac9 influenza b
539	35	46.7	326	2	Q8JMP2_9INFB	q8jmp2 influenza b
540	35	46.7	326	2	Q8JMP3_9INFB	q8jmp3 influenza b
541	35	46.7	326	2	Q8JMP2_9INFB	q8jmp2 influenza b
542	35	46.7	326	2	Q8JMP4_9INFB	q8jmp4 influenza b

No.			Len	n	Accession	id	Organism
543	35	46.7	326	2	Q8JY85_9INFB	Q8jy85	influenza b
544	35	46.7	326	2	Q8JY86_9INFB	Q8jy86	influenza b
545	35	46.7	326	2	Q8JY87_9INFB	Q8jy87	influenza b
546	35	46.7	326	2	Q8JY88_9INFB	Q8jy88	influenza b
547	35	46.7	326	2	Q8JY89_9INFB	Q8jy89	influenza b
548	35	46.7	326	2	Q8JY90_9INFB	Q8jy90	influenza b
549	35	46.7	326	2	Q8JY92_9INFB	Q8jy92	influenza b
550	35	46.7	326	2	Q8JY93_9INFB	Q8jy93	influenza b
551	35	46.7	328	2	Q8QVK2_9INFB	Q8qvk2	influenza b
552	35	46.7	329	2	Q8QVK2_9INFB	Q8qvk2	influenza b
553	35	46.7	329	2	Q925X0_RHIME	Q925x0	rhizobium m
554	35	46.7	329	2	Q8QVK7_9INFB	Q8qvk7	influenza b
555	35	46.7	331	2	Q9QAV7_9INFB	Q9qav7	influenza b
556	35	46.7	331	2	Q41CQ9_9INFB	Q41cq9	influenza b
557	35	46.7	332	2	Q52G68_9INFB	Q52g68	influenza b
558	35	46.7	332	2	Q52G69_9INFB	Q52g69	influenza b
559	35	46.7	332	2	Q52G70_9INFB	Q52g70	influenza b
560	35	46.7	332	2	Q52G71_9INFB	Q52g71	influenza b
561	35	46.7	332	2	Q52G72_9INFB	Q52g72	influenza b
562	35	46.7	332	2	Q52G73_9INFB	Q52g73	influenza b
563	35	46.7	332	2	Q52G74_9INFB	Q52g74	influenza b
564	35	46.7	332	2	Q52G75_9INFB	Q52g75	influenza b
565	35	46.7	332	2	Q52G76_9INFB	Q52g76	influenza b
566	35	46.7	332	2	Q52G77_9INFB	Q52g77	influenza b
567	35	46.7	333	2	Q52G78_9INFB	Q52g78	influenza b
568	35	46.7	333	2	Q52G79_9INFB	Q52g79	influenza b
569	35	46.7	333	2	Q52G80_9INFB	Q52g80	influenza b
570	35	46.7	333	2	Q52G81_9INFB	Q52g81	influenza b
571	35	46.7	333	2	Q52G82_9INFB	Q52g82	influenza b
572	35	46.7	333	2	Q52G83_9INFB	Q52g83	influenza b
573	35	46.7	333	2	Q52G84_9INFB	Q52g84	influenza b
574	35	46.7	333	2	Q52G85_9INFB	Q52g85	influenza b
575	35	46.7	333	2	Q52G86_9INFB	Q52g86	influenza b
576	35	46.7	333	2	Q52G87_9INFB	Q52g87	influenza b
577	35	46.7	333	2	Q52G88_9INFB	Q52g88	influenza b
578	35	46.7	333	2	Q52G89_9INFB	Q52g89	influenza b
579	35	46.7	333	2	Q52G90_9INFB	Q52g90	influenza b
580	35	46.7	333	2	Q52G91_9INFB	Q52g91	influenza b
581	35	46.7	333	2	Q52G92_9INFB	Q52g92	influenza b
582	35	46.7	333	2	Q52G93_9INFB	Q52g93	influenza b
583	35	46.7	333	2	Q52G94_9INFB	Q52g94	influenza b
584	35	46.7	333	2	Q52G96_9INFB	Q52g96	influenza b
585	35	46.7	333	2	Q52G97_9INFB	Q52g97	influenza b
586	35	46.7	333	2	Q52G98_9INFB	Q52g98	influenza b
587	35	46.7	333	2	Q52G99_9INFB	Q52g99	influenza b
588	35	46.7	333	2	Q80ST0_9INFB	Q80st0	influenza b
589	35	46.7	333	2	Q80ST1_9INFB	Q80st1	influenza b
590	35	46.7	333	2	Q80ST2_9INFB	Q80st2	influenza b
591	35	46.7	333	2	Q80ST5_9INFB	Q80st5	influenza b
592	35	46.7	333	2	Q80ST6_9INFB	Q80st6	influenza b
593	35	46.7	333	2	Q80ST7_9INFB	Q80st7	influenza b
594	35	46.7	333	2	Q80ST8_9INFB	Q80st8	influenza b
595	35	46.7	333	2	Q80ST9_9INFB	Q80st9	influenza b
596	35	46.7	333	2	Q80SU0_9INFB	Q80su0	influenza b
597	35	46.7	333	2	Q80SU1_9INFB	Q80su1	influenza b
598	35	46.7	333	2	Q80SU2_9INFB	Q80su2	influenza b
599	35	46.7	333	2	Q80SU3_9INFB	Q80su3	influenza b
600	35	46.7	333	2	Q80SU4_9INFB	Q80su4	influenza b
601	35	46.7	333	2	Q80SU5_9INFB	Q80su5	influenza b
602	35	46.7	333	2	Q80SU6_9INFB	Q80su6	influenza b
603	35	46.7	333	2	Q80SU7_9INFB	Q80su7	influenza b
604	35	46.7	333	2	Q80SU8_9INFB	Q80su8	influenza b
605	35	46.7	333	2	Q80SU9_9INFB	Q80su9	influenza b
606	35	46.7	334	2	Q6MOP4_METMP	Q6mop4	methanococc
607	35	46.7	334	2	Q75T71_9INFB	Q75t71	influenza b
608	35	46.7	334	2	Q80SS2_9INFB	Q80ss2	influenza b
609	35	46.7	334	2	Q80SS3_9INFB	Q80ss3	influenza b
610	35	46.7	334	2	Q80SS4_9INFB	Q80ss4	influenza b
611	35	46.7	334	2	Q80SS5_9INFB	Q80ss5	influenza b
612	35	46.7	334	2	Q80SS6_9INFB	Q80ss6	influenza b
613	35	46.7	334	2	Q80SS7_9INFB	Q80ss7	influenza b
614	35	46.7	334	2	Q80SS8_9INFB	Q80ss8	influenza b
615	35	46.7	334	2	Q80SS9_9INFB	Q80ss9	influenza b
616	35	46.7	334	2	Q80ST4_9INFB	Q80st4	influenza b
617	35	46.7	334	2	Q80SV0_9INFB	Q80sv0	influenza b
618	35	46.7	334	2	Q80SV1_9INFB	Q80sv1	influenza b
619	35	46.7	335	2	Q5R1N7_9INFB	Q5r1n7	influenza b
620	35	46.7	335	2	Q5R1N8_9INFB	Q5r1n8	influenza b
621	35	46.7	335	2	Q75T70_9INFB	Q75t70	influenza b
622	35	46.7	335	2	Q75T75_9INFB	Q75t75	influenza b
623	35	46.7	335	2	Q75T76_9INFB	Q75t76	influenza b
624	35	46.7	335	2	Q75T77_9INFB	Q75t77	influenza b
625	35	46.7	335	2	Q9QAV5_9INFB	Q9qav5	influenza b
626	35	46.7	335	2	Q9QAV6_9INFB	Q9qav6	influenza b
627	35	46.7	335	2	Q9QAV8_9INFB	Q9qav8	influenza b
628	35	46.7	335	2	Q5R1N9_9INFB	Q5r1n9	influenza b
629	35	46.7	335	2	Q75T78_9INFB	Q75t78	influenza b
630	35	46.7	336	2	Q9QAV1_9INFB	Q9qav1	influenza b
631	35	46.7	336	2	Q5A5Q4_CANAL	Q5a5q4	candida alb
632	35	46.7	336	2	Q4LCS0_9INFB	Q4lcs0	influenza b
633	35	46.7	339	2	Q41CQ4_9INFB	Q41cq4	influenza b
634	35	46.7	339	2	Q41CQ9_9INFB	Q41cq9	influenza b
635	35	46.7	342	2	Q8JP22_9INFB	Q8jp22	influenza b
636	35	46.7	343	2	Q91NG7_9INFB	Q91ng7	influenza b
637	35	46.7	344	2	Q91NG8_9INFB	Q91ng8	influenza b
638	35	46.7	344	2	Q9QMU2_9INFB	Q9qmu2	influenza b
639	35	46.7	344	2	Q9QMU5_9INFB	Q9qmu5	influenza b
640	35	46.7	344	2	Q9WDB0_9INFB	Q9wdb0	influenza b
641	35	46.7	344	1	Q4LCR4_9INFB	Q4lcr4	influenza b
642	35	46.7	345	1	HEMA_INBFU	HEMA_INBFU	influenza b
643	35	46.7	345	2	P18877	P18877	influenza b
644	35	46.7	345	2	Q4PEF7_USTMA	Q4pef7	ustilago ma
645	35	46.7	345	2	Q8C237_MOUSE	Q8c237	mus musculu
646	35	46.7	345	2	Q71CC5_9INFB	Q71cc5	influenza b
647	35	46.7	345	2	Q71CC6_9INFB	Q71cc6	influenza b
648	35	46.7	345	2	Q71CC7_9INFB	Q71cc7	influenza b
649	35	46.7	345	2	Q71CC8_9INFB	Q71cc8	influenza b
650	35	46.7	345	2	Q71CC9_9INFB	Q71cc9	influenza b
651	35	46.7	345	2	Q71CD0_9INFB	Q71cd0	influenza b
652	35	46.7	345	2	Q71CD1_9INFB	Q71cd1	influenza b
653	35	46.7	345	2	Q77WX6_9INFB	Q77wx6	influenza b
654	35	46.7	345	2	O82638_9INFB	082638	influenza b
655	35	46.7	345	2	O82639_9INFB	082639	influenza b
656	35	46.7	345	2	O82640_9INFB	082640	influenza b
657	35	46.7	345	2	O82641_9INFB	082641	influenza b
658	35	46.7	345	2	O82642_9INFB	082642	influenza b
659	35	46.7	345	2	O82643_9INFB	082643	influenza b
660	35	46.7	345	2	O82645_9INFB	082645	influenza b
661	35	46.7	345	2	O82647_9INFB	082647	influenza b
662	35	46.7	345	2	O82648_9INFB	082648	influenza b
663	35	46.7	345	2	O82652_9INFB	082652	influenza b
664	35	46.7	345	2	O82653_9INFB	082653	influenza b
665	35	46.7	345	2	O82655_9INFB	082655	influenza b
666	35	46.7	345	2	O82825_9INFB	082825	influenza b
667	35	46.7	345	2	Q8B9Z1_9INFB	Q8b9z1	influenza b
668	35	46.7	345	2	Q8JK24_9INFB	Q8jk24	influenza b
669	35	46.7	345	2	Q8JK26_9INFB	Q8jk26	influenza b
670	35	46.7	345	2	Q8JP19_9INFB	Q8jp19	influenza b
671	35	46.7	345	2	Q91NF6_9INFB	Q91nf6	influenza b
672	35	46.7	345	2	Q91NF9_9INFB	Q91nf9	influenza b
673	35	46.7	345	2	Q91NG0_9INFB	Q91ng0	influenza b
674	35	46.7	345	2	Q91NG4_9INFB	Q91ng4	influenza b
675	35	46.7	345	2	Q91NG5_9INFB	Q91ng5	influenza b
676	35	46.7	345	2	Q91NG6_9INFB	Q91ng6	influenza b
677	35	46.7	345	2	Q9QMS4_9INFB	Q9qms4	influenza b
678	35	46.7	345	2	Q9QMT7_9INFB	Q9qmt7	influenza b
679	35	46.7	345	2	Q9QMU0_9INFB	Q9qmu0	influenza b
680	35	46.7	345	2	Q9QMU1_9INFB	Q9qmu1	influenza b
681	35	46.7	345	2	Q9QMU7_9INFB	Q9qmu7	influenza b
682	35	46.7	345	2	Q9WDA9_9INFB	Q9wda9	influenza b
683	35	46.7	345	2	Q9WDB2_9INFB	Q9wdb2	influenza b
684	35	46.7	345	2	Q9WDB3_9INFB	Q9wdb3	influenza b
685	35	46.7	345	2	Q9YIL8_9INFB	Q9yil8	influenza b
686	35	46.7	345	2	Q9YWG8_9INFB	Q9ywg8	influenza b
687	35	46.7	345	2	Q9YWG9_9INFB	Q9ywg9	influenza b
688	35	46.7	345	2	Q9YWH0_9INFB	Q9ywh0	influenza b

No.					ID (_9INFB)	Accession	Organism
689	35	46.7	345	2	Q9YWH2_9INFB	Q9ywh2	influenza b
690	35	46.7	345	2	Q9YWH3_9INFB	Q9ywh3	influenza b
691	35	46.7	345	2	Q9YWH4_9INFB	Q9ywh4	influenza b
692	35	46.7	345	2	Q9YWH5_9INFB	Q9ywh5	influenza b
693	35	46.7	345	2	Q9YWH6_9INFB	Q9ywh6	influenza b
694	35	46.7	345	2	Q9YWH7_9INFB	Q9ywh7	influenza b
695	35	46.7	345	2	Q9YWH8_9INFB	Q9ywh8	influenza b
696	35	46.7	345	2	Q9YWH9_9INFB	Q9ywh9	influenza b
697	35	46.7	345	2	Q9YWI0_9INFB	Q9ywi0	influenza b
698	35	46.7	345	2	Q9YWI1_9INFB	Q9ywi1	influenza b
699	35	46.7	345	2	Q9YWI2_9INFB	Q9ywi2	influenza b
700	35	46.7	345	2	Q9YWI3_9INFB	Q9ywi3	influenza b
701	35	46.7	345	2	Q9YWI4_9INFB	Q9ywi4	influenza b
702	35	46.7	345	2	Q9YWI5_9INFB	Q9ywi5	influenza b
703	35	46.7	345	2	Q9YWI6_9INFB	Q9ywi6	influenza b
704	35	46.7	345	2	Q9YWI7_9INFB	Q9ywi7	influenza b
705	35	46.7	345	2	Q9YWI8_9INFB	Q9ywi8	influenza b
706	35	46.7	345	2	Q9YWI9_9INFB	Q9ywi9	influenza b
707	35	46.7	345	2	Q9YWJ0_9INFB	Q9ywj0	influenza b
708	35	46.7	345	2	Q9YWJ1_9INFB	Q9ywj1	influenza b
709	35	46.7	345	2	Q9YWJ2_9INFB	Q9ywj2	influenza b
710	35	46.7	345	2	Q9YWJ3_9INFB	Q9ywj3	influenza b
711	35	46.7	345	2	Q9YWJ4_9INFB	Q9ywj4	influenza b
712	35	46.7	345	2	Q9YWJ5_9INFB	Q9ywj5	influenza b
713	35	46.7	345	2	Q9YWJ6_9INFB	Q9ywj6	influenza b
714	35	46.7	345	2	Q9YWJ7_9INFB	Q9ywj7	influenza b
715	35	46.7	345	2	Q9YWJ8_9INFB	Q9ywj8	influenza b
716	35	46.7	345	2	Q4LCR0_9INFB	Q4lcr0	influenza b
717	35	46.7	345	2	Q4LCS1_9INFB	Q4lcs1	influenza b
718	35	46.7	345	2	Q4LCQ7_9INFB	Q4lcq7	influenza b
719	35	46.7	345	2	Q5XPB6_9INFB	Q5xpb6	influenza b
720	35	46.7	345	2	Q5XPB7_9INFB	Q5xpb7	influenza b
721	35	46.7	345	2	Q5XPB8_9INFB	Q5xpb8	influenza b
722	35	46.7	345	2	Q5XPB9_9INFB	Q5xpb9	influenza b
723	35	46.7	345	2	Q5XPC0_9INFB	Q5xpc0	influenza b
724	35	46.7	345	2	Q5XPC1_9INFB	Q5xpc1	influenza b
725	35	46.7	345	2	Q5XPC2_9INFB	Q5xpc2	influenza b
726	35	46.7	345	2	Q5XPC3_9INFB	Q5xpc3	influenza b
727	35	46.7	345	2	O60H70_9INFB	O60h70	influenza b
728	35	46.7	345	2	O60H71_9INFB	O60h71	influenza b
729	35	46.7	345	2	O60H72_9INFB	O60h72	influenza b
730	35	46.7	345	2	O60H73_9INFB	O60h73	influenza b
731	35	46.7	345	2	Q6F4N9_9INFB	Q6f4n9	influenza b
732	35	46.7	345	2	Q6F4P0_9INFB	Q6f4p0	influenza b
733	35	46.7	345	2	Q6F4P3_9INFB	Q6f4p3	influenza b
734	35	46.7	345	2	Q6F4P4_9INFB	Q6f4p4	influenza b
735	35	46.7	345	2	Q6F4P5_9INFB	Q6f4p5	influenza b
736	35	46.7	345	2	Q6F4P6_9INFB	Q6f4p6	influenza b
737	35	46.7	345	2	Q6F4P7_9INFB	Q6f4p7	influenza b
738	35	46.7	345	2	Q6F4P8_9INFB	Q6f4p8	influenza b
739	35	46.7	345	2	Q6F4P9_9INFB	Q6f4p9	influenza b
740	35	46.7	345	2	Q6F4Q0_9INFB	Q6f4q0	influenza b
741	35	46.7	345	2	Q6F4Q1_9INFB	Q6f4q1	influenza b
742	35	46.7	345	2	Q6F4Q2_9INFB	Q6f4q2	influenza b
743	35	46.7	345	2	Q6F4Q3_9INFB	Q6f4q3	influenza b
744	35	46.7	345	2	Q6F4Q4_9INFB	Q6f4q4	influenza b
745	35	46.7	345	2	Q6F4Q5_9INFB	Q6f4q5	influenza b
746	35	46.7	345	2	Q6F4Q6_9INFB	Q6f4q6	influenza b
747	35	46.7	345	2	Q6F4Q7_9INFB	Q6f4q7	influenza b
748	35	46.7	345	2	Q6F4Q8_9INFB	Q6f4q8	influenza b
749	35	46.7	345	2	Q6F4Q9_9INFB	Q6f4q9	influenza b
750	35	46.7	345	2	Q6F4R0_9INFB	Q6f4r0	influenza b
751	35	46.7	345	2	Q6F4R1_9INFB	Q6f4r1	influenza b
752	35	46.7	345	2	Q6F4R2_9INFB	Q6f4r2	influenza b
753	35	46.7	345	2	Q71CC2_9INFB	Q71cc2	influenza b
754	35	46.7	345	2	Q71CC3_9INFB	Q71cc3	influenza b
755	35	46.7	345	2	Q71CC4_9INFB	Q71cc4	influenza b
756	35	46.7	345	2	Q77WW2_9INFB	Q77ww2	influenza b
757	35	46.7	345	2	Q77WW3_9INFB	Q77ww3	influenza b
758	35	46.7	345	2	Q77WW4_9INFB	Q77ww4	influenza b
759	35	46.7	345	2	Q77WW5_9INFB	Q77ww5	influenza b
760	35	46.7	345	2	Q77WW6_9INFB	Q77ww6	influenza b
761	35	46.7	346	2	Q77WW7_9INFB	Q77ww7	influenza b

No.					ID (_9INFB)	Accession	Organism
762	35	46.7	346	2	Q77WW8_9INFB	Q77ww8	influenza b
763	35	46.7	346	2	Q77WW9_9INFB	Q77ww9	influenza b
764	35	46.7	346	2	Q77WX0_9INFB	Q77wx0	influenza b
765	35	46.7	346	2	Q77WX1_9INFB	Q77wx1	influenza b
766	35	46.7	346	2	Q77WX2_9INFB	Q77wx2	influenza b
767	35	46.7	346	2	Q77WX3_9INFB	Q77wx3	influenza b
768	35	46.7	346	2	Q77WX4_9INFB	Q77wx4	influenza b
769	35	46.7	346	2	Q77WX5_9INFB	Q77wx5	influenza b
770	35	46.7	346	2	Q8B9Z4_9INFB	Q8b9z4	influenza b
771	35	46.7	346	2	Q8B9Z5_9INFB	Q8b9z5	influenza b
772	35	46.7	346	2	Q8B9Z8_9INFB	Q8b9z8	influenza b
773	35	46.7	346	2	O8VG30_9INFB	O8vg30	influenza b
774	35	46.7	346	2	O8JP31_9INFB	O8jp31	influenza b
775	35	46.7	346	2	Q9IIY6_9INFB	Q9iiy6	influenza b
776	35	46.7	346	2	Q9IIY7_9INFB	Q9iiy7	influenza b
777	35	46.7	346	2	Q9IIY8_9INFB	Q9iiy8	influenza b
778	35	46.7	346	2	Q9IIY9_9INFB	Q9iiy9	influenza b
779	35	46.7	346	2	Q9IIZ0_9INFB	Q9iiz0	influenza b
780	35	46.7	346	2	Q9IIZ1_9INFB	Q9iiz1	influenza b
781	35	46.7	346	2	Q9IIZ2_9INFB	Q9iiz2	influenza b
782	35	46.7	346	2	Q9IIZ3_9INFB	Q9iiz3	influenza b
783	35	46.7	346	2	Q9IIZ4_9INFB	Q9iiz4	influenza b
784	35	46.7	346	2	Q9IIZ5_9INFB	Q9iiz5	influenza b
785	35	46.7	346	2	Q9IIZ6_9INFB	Q9iiz6	influenza b
786	35	46.7	346	2	Q9IIZ7_9INFB	Q9iiz7	influenza b
787	35	46.7	346	2	Q9IIZ8_9INFB	Q9iiz8	influenza b
788	35	46.7	346	2	Q9IIZ9_9INFB	Q9iiz9	influenza b
789	35	46.7	346	2	Q9I2A0_9INFB	Q9i2a0	influenza b
790	35	46.7	346	2	Q9I2A1_9INFB	Q9i2a1	influenza b
791	35	46.7	346	2	Q9I2A2_9INFB	Q9i2a2	influenza b
792	35	46.7	346	2	Q9I2A3_9INFB	Q9i2a3	influenza b
793	35	46.7	346	2	Q9I2A4_9INFB	Q9i2a4	influenza b
794	35	46.7	346	2	Q9I2A6_9INFB	Q9i2a6	influenza b
795	35	46.7	346	2	Q91NF2_9INFB	Q91nf2	influenza b
796	35	46.7	346	2	Q91NG3_9INFB	Q91ng3	influenza b
797	35	46.7	346	2	Q91IQ4_9INFB	Q91iq4	influenza b
798	35	46.7	346	2	Q91IQ5_9INFB	Q91iq5	influenza b
799	35	46.7	346	2	Q91IR0_9INFB	Q91ir0	influenza b
800	35	46.7	346	2	Q91IS6_9INFB	Q91is6	influenza b
801	35	46.7	346	2	Q90MU4_9INFB	Q90mu4	influenza b
802	35	46.7	346	2	Q9QMU3_9INFB	Q9qmu3	influenza b
803	35	46.7	346	2	Q9WD49_9INFB	Q9wd49	influenza b
804	35	46.7	346	2	Q9WD51_9INFB	Q9wd51	influenza b
805	35	46.7	346	2	Q9WD52_9INFB	Q9wd52	influenza b
806	35	46.7	346	2	Q9WD55_9INFB	Q9wd55	influenza b
807	35	46.7	346	2	Q9WD56_9INFB	Q9wd56	influenza b
808	35	46.7	346	2	Q9WDA8_9INFB	Q9wda8	influenza b
809	35	46.7	346	2	Q9IP7_9INFB	Q9ip7	influenza b
810	35	46.7	346	2	Q9IS6_9INFB	Q9is6	influenza b
811	35	46.7	346	2	Q9IV4_9INFB	Q9iv4	influenza b
812	35	46.7	346	2	Q9IT2_9INFB	Q9it2	influenza b
813	35	46.7	346	2	Q9IC6_9INFB	Q9ic6	influenza b
814	35	46.7	346	2	Q9VJB3_9INFB	Q9vjb3	influenza b
815	35	46.7	346	2	Q9VJG2_9INFB	Q9vjg2	influenza b
816	35	46.7	346	2	Q9VIF9_9INFB	Q9vif9	influenza b
817	35	46.7	346	2	Q9VIC6_9INFB	Q9vic6	influenza b
818	35	46.7	346	2	Q9VIJ12_9INFB	Q9vij12	influenza b
819	35	46.7	346	2	Q9YNC1_9INFB	Q9ync1	influenza b
820	35	46.7	346	2	Q9YNC2_9INFB	Q9ync2	influenza b
821	35	46.7	346	2	Q9YNC3_9INFB	Q9ync3	influenza b
822	35	46.7	346	2	Q9YNC4_9INFB	Q9ync4	influenza b
823	35	46.7	346	2	Q9YNC5_9INFB	Q9ync5	influenza b
824	35	46.7	346	2	Q9YNC6_9INFB	Q9ync6	influenza b
825	35	46.7	346	2	Q9YNC7_9INFB	Q9ync7	influenza b
826	35	46.7	346	2	Q9YNC8_9INFB	Q9ync8	influenza b
827	35	46.7	346	2	Q9YNC9_9INFB	Q9ync9	influenza b
828	35	46.7	346	2	Q9YWD0_9INFB	Q9ywd0	influenza b
829	35	46.7	346	2	Q9YWD1_9INFB	Q9ywd1	influenza b
830	35	46.7	346	2	Q9YWD2_9INFB	Q9ywd2	influenza b
831	35	46.7	346	2	Q9YWD3_9INFB	Q9ywd3	influenza b
832	35	46.7	346	2	Q9YWD4_9INFB	Q9ywd4	influenza b
833	35	46.7	346	2	Q9YWD5_9INFB	Q9ywd5	influenza b
834	35	46.7	346	2	Q9YWD6_9INFB	Q9ywd6	influenza b

Left listing:

#					Name	Accession	Organism
835	35	46.7	346	2	Q9YWD9_9INFB	q9ywd9	influenza b
836	35	46.7	346	2	Q9YWE0_9INFB	q9ywe0	influenza b
837	35	46.7	346	2	Q9YWE1_9INFB	q9ywe1	influenza b
838	35	46.7	346	2	Q9YWE2_9INFB	q9ywe2	influenza b
839	35	46.7	346	2	Q9YWE3_9INFB	q9ywe3	influenza b
840	35	46.7	346	2	Q9YWE4_9INFB	q9ywe4	influenza b
841	35	46.7	346	2	Q9YWE5_9INFB	q9ywe5	influenza b
842	35	46.7	346	2	Q9YWE6_9INFB	q9ywe6	influenza b
843	35	46.7	346	2	Q9YWE7_9INFB	q9ywe7	influenza b
844	35	46.7	346	2	Q9YWE8_9INFB	q9ywe8	influenza b
845	35	46.7	346	2	Q9YWE9_9INFB	q9ywe9	influenza b
846	35	46.7	346	2	Q9YWF0_9INFB	q9ywf0	influenza b
847	35	46.7	346	2	Q9YWF1_9INFB	q9ywf1	influenza b
848	35	46.7	346	2	Q9YWF2_9INFB	q9ywf2	influenza b
849	35	46.7	346	2	Q9YWF3_9INFB	q9ywf3	influenza b
850	35	46.7	346	2	Q9YWF4_9INFB	q9ywf4	influenza b
851	35	46.7	346	2	Q9YWF5_9INFB	q9ywf5	influenza b
852	35	46.7	346	2	Q9YWF6_9INFB	q9ywf6	influenza b
853	35	46.7	346	2	Q9YWF7_9INFB	q9ywf7	influenza b
854	35	46.7	346	2	Q9YWF8_9INFB	q9ywf8	influenza b
855	35	46.7	346	2	Q9YWF9_9INFB	q9ywf9	influenza b
856	35	46.7	346	2	Q9YWG0_9INFB	q9ywg0	influenza b
857	35	46.7	346	2	Q9YWG1_9INFB	q9ywg1	influenza b
858	35	46.7	346	2	Q9YWG2_9INFB	q9ywg2	influenza b
859	35	46.7	346	2	Q9YWG3_9INFB	q9ywg3	influenza b
860	35	46.7	346	2	Q9YWG4_9INFB	q9ywg4	influenza b
861	35	46.7	346	2	Q9YWG5_9INFB	q9ywg5	influenza b
862	35	46.7	346	2	Q9YWG6_9INFB	q9ywg6	influenza b
863	35	46.7	346	2	Q9YWG7_9INFB	q9ywg7	influenza b
864	35	46.7	346	2	Q4LCR2_9INFB	q4lcr2	influenza b
865	35	46.7	347	1	HEMA_INBF1	O07925	influenza b
866	35	46.7	347	1	HEMA_INBF2	O07926	influenza b
867	35	46.7	347	1	HEMA_INBF3	P68755	influenza b
868	35	46.7	347	1	HEMA_INBF4	P68756	influenza b
869	35	46.7	347	1	HEMA_INBF5	P68757	influenza b
870	35	46.7	347	1	HEMA_INBF6	P68758	influenza b
871	35	46.7	347	1	HEMA_INBF7	P68759	influenza b
872	35	46.7	347	1	HEMA_INBF8	P68760	influenza b
873	35	46.7	347	1	HEMA_INBF9	O07920	influenza b
874	35	46.7	347	1	HEMA_INBIB	P18878	influenza b
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876	35	46.7	347	1	Q9FFM1_ARATH	q9ffm1	arabidopsis
877	35	46.7	347	1	P18879_ARATH	p18879	arabidopsis
878	35	46.7	347	2	Q5XPC1_9INFB	q5xpc1	influenza b
879	35	46.7	347	2	Q5XPC2_9INFB	q5xpc2	influenza b
880	35	46.7	347	2	Q5XPC3_9INFB	q5xpc3	influenza b
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883	35	46.7	347	2	Q5XPC6_9INFB	q5xpc6	influenza b
884	35	46.7	347	2	Q5XPC7_9INFB	q5xpc7	influenza b
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886	35	46.7	347	2	Q5XPC9_9INFB	q5xpc9	influenza b
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888	35	46.7	347	2	Q5XPD1_9INFB	q5xpd1	influenza b
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891	35	46.7	347	2	Q5XPD4_9INFB	q5xpd4	influenza b
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893	35	46.7	347	2	Q5XPD6_9INFB	q5xpd6	influenza b
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895	35	46.7	347	2	Q5XPD8_9INFB	q5xpd8	influenza b
896	35	46.7	347	2	Q5XPD9_9INFB	q5xpd9	influenza b
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898	35	46.7	347	2	Q5XPE1_9INFB	q5xpe1	influenza b
899	35	46.7	347	2	Q5XPE2_9INFB	q5xpe2	influenza b
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901	35	46.7	347	2	Q5XPE4_9INFB	q5xpe4	influenza b
902	35	46.7	347	2	Q5XPE7_9INFB	q5xpe7	influenza b
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904	35	46.7	347	2	Q5XPE9_9INFB	q5xpe9	influenza b
905	35	46.7	347	2	Q5XPF0_9INFB	q5xpf0	influenza b
906	35	46.7	347	2	Q60H78_9INFB	q60h78	influenza b
907	35	46.7	347	2	Q60H79_9INFB	q60h79	influenza b

Right listing:

#					Name	Accession	Organism
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910	35	46.7	347	2	Q6F4P2_9INFB	q6f4p2	influenza b
911	35	46.7	347	2	Q77SV0_9INFB	q77sv0	influenza b
912	35	46.7	347	2	O82636_9INFB	o82636	influenza b
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914	35	46.7	347	2	O82644_9INFB	o82644	influenza b
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929	35	46.7	347	2	O8JP28_9INFB	o8jp28	influenza b
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963	35	46.7	350	2	O8JP26_9INFB	o8jp26	influenza b
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974	35	46.7	351	2	O80RD1_9INFB	o80rd1	influenza b
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976	35	46.7	351	2	O8JP32_9INFB	o8jp32	influenza b
977	35	46.7	351	2	O8JP38_9INFB	o8jp38	influenza b
978	35	46.7	351	2	O8JP42_9INFB	o8jp42	influenza b
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ALIGNMENTS

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982   35  46.7  352  2  Q8B9Y9_9INFB   Q8b9y9  influenza b
983   35  46.7  352  2  Q8B9Z2_9INFB   Q8b9z2  influenza b
984   35  46.7  352  2  Q8JP18_9INFB   Q8jp18  influenza b
985   35  46.7  352  2  Q8JP21_9INFB   Q8jp21  influenza b
986   35  46.7  352  2  Q8JP25_9INFB   Q8jp25  influenza b
987   35  46.7  352  2  Q8JP29_9INFB   Q8jp29  influenza b
988   35  46.7  352  2  Q8JP39_9INFB   Q8jp39  influenza b
989   35  46.7  352  2  Q8JP40_9INFB   Q8jp40  influenza b
990   35  46.7  352  2  Q8JP54_9INFB   Q8jp54  influenza b
991   35  46.7  352  2  Q99162_9INFB   Q99162  influenza b
992   35  46.7  352  2  Q9QKD7_9INFB   Q9qkd7  influenza b
993   35  46.7  352  2  Q9QKD8_9INFB   Q9qkd8  influenza b
994   35  46.7  352  2  Q9QKD9_9INFB   Q9qkd9  influenza b
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996   35  46.7  353  1  HEMA_INBAA     P12440  influenza b
997   35  46.7  353  2  Q8JP30_9INFB   Q8jp30  influenza b
998   35  46.7  353  2  Q8JP47_9INFB   Q8jp47  influenza b
999   35  46.7  353  2  Q91CN9_9INFB   Q91cn9  influenza b
1000  35  46.7  353  2  Q9QMH0_9INFB   Q9qmh0  influenza b
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RESULT 1

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ID   FA8_HUMAN   STANDARD;   PRT;   2351 AA.
AC   P00451;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Coagulation factor VIII precursor (Procoagulant component)
DE   (Antihemophilic factor) (AHF) (Contains: Factor VIIIa heavy chain, 200
DE   kDa isoform; Factor VIIIa heavy chain, 92 kDa isoform; Factor VIII B
DE   chain; Factor VIIIa light chain).
GN   Name=F8; Synonyms=F8C;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=86081164; PubMed=3935400;
RA   Truett M.A., Blacher R., Burke R.L., Caput D., Chu C., Dina D.,
RA   Hartog K., Kuo C.H., Masiarz F.R., Merryweather J.P., Najarian R.,
RA   Pachl C., Potter S.J., Puma J., Quiroga M., Rall L.B., Randolph A.,
RA   Urdea M.S., Valenzuela P., Dahl H.-H.M., Favaloro J., Hansen J.,
RA   Nordfang O., Ezban M.;
RT   "Characterization of the polypeptide composition of human factor
RT   VIII:C and the nucleotide sequence and expression of the human factor
RT   VIII cDNA.";
RL   DNA 4:333-349(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=85061550; PubMed=6438528;
RA   Toole J.J., Knopf J.L., Wozney J.M., Sultzman L.A., Buecker J.L.,
RA   Pittman D.D., Kaufman R.J., Brown E., Shoemaker C., Orr E.C.,
RA   Amphlett G.W., Foster W.B., Coe M.L., Knutson G.J., Fass D.N.,
RA   Hewick R.M.;
RT   "Molecular cloning of a cDNA encoding human antihaemophilic factor.";
RL   Nature 312:342-347(1984).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=85061548; PubMed=6438526;
RA   Wood W.I., Capon D.J., Simonsen C.C., Eaton D.L., Gitschier J.,
RA   Keyt B., Seeburg P.H., Smith D.H., Hollingshead P., Wion K.L.,
RA   Delwart E., Tuddenham E.G.D., Vehar G.A., Lawn R.M.;
RT   "Expression of active human factor VIII from recombinant DNA clones.";
RL   Nature 312:330-337(1984).
RN   [4]
RP   NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RX   MEDLINE=93265012; PubMed=1303178;
RA   Gitschier J., Wood W.I.;
RT   "Sequence of the exon-containing regions of the human factor VIII
RT   gene.";
RL   Hum. Mol. Genet. 1:199-200(1992).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLU-1260 AND VAL-2257.
RX   MEDLINE=92207952; PubMed=1554716;
RA   Pittman D.D., Wang J.H., Kaufman R.J.;
RT   "Identification and functional importance of tyrosine sulfate residues
RT   within recombinant factor VIII.";
RL   Biochemistry 31:3315-3325(1992).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA   Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA   Rajkumar R., Yi Q., Nickerson D.A.;
RT   "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 2064-2070.
RA   de Water N.S., Williams R., Browett P.J.;
RT   "Factor VIII gene normal intron 20 sequence.";
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   SULFATION OF TYR-1699.
RX   MEDLINE=91093266; PubMed=1898735;
RA   Leyte A., van Schijndel H.B., Niehrs C., Huttner W.B., Verbeet M.P.,
RA   Mertens K., van Mourik J.A.;
RT   "Sulfation of Tyr1680 of human blood coagulation factor VIII is
RT   essential for the interaction of factor VIII with von Willebrand
RT   factor.";
RL   J. Biol. Chem. 266:740-746(1991).
RN   [9]
RP   SULFATION SITES TYR-737; TYR-738 AND TYR 742, AND DISULFIDE BONDS.
RX   MEDLINE=95338127; PubMed=7613471;
RA   McMullen B.A., Fujikawa K., Davie E.W., Hedner U., Ezban M.;
RT   "Locations of disulfide bonds and free cysteines in the heavy and
RT   light chains of recombinant human factor VIII (antihemophilic factor
RT   A).";
RL   Protein Sci. 4:740-746(1995).
RN   [10]
RP   STRUCTURE BY NMR OF 2322-2343.
RX   MEDLINE=95209924; PubMed=7893714;
RA   Gilbert G.E., Baleja J.D.;
RT   "Membrane-binding peptide from the C2 domain of factor VIII forms an
RT   amphipathic structure as determined by NMR spectroscopy.";
RL   Biochemistry 34:3022-3031(1995).
RN   [11]
RP   REVIEW ON MOLECULAR BASIS OF HEMA.
RX   MEDLINE=91221499; PubMed=1902642;
RA   Gitschier J.;
RT   "The molecular basis of hemophilia A.";
RL   Ann. N. Y. Acad. Sci. 614:89-96(1991).
RN   [12]
RP   REVIEW ON MOLECULAR BASIS OF HEMA.
RX   MEDLINE=89088506; PubMed=2491949;
RA   White G.C. II, Shoemaker C.B.;
RT   "Factor VIII gene and hemophilia A.";
RL   Blood 73:1-12(1989).
RN   [13]
RP   REVIEW ON MOLECULAR BASIS OF HEMA.
RX   MEDLINE=95245332; PubMed=7728145;
RA   Antonarakis S.E., Kazazian H.H. Jr., Tuddenham E.G.D.;
RT   "Molecular etiology of factor VIII deficiency in hemophilia A.";
RL   Hum. Mutat. 5:1-22(1995).
RN   [14]
RP   VARIANT HEMA GLN-2326.
RX   MEDLINE=86235434; PubMed=3012775;
RA   Gitschier J., Wood W.I., Shuman M.A., Lawn R.M.;
RT   "Identification of a missense mutation in the factor VIII gene of a
RT   mild hemophiliac.";
RL   Science 232:1415-1416(1986).
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OM protein - protein search, using sw model

GenCore version 5.1.6
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Title:	US-10-511-559-73_COPY_817_831
Perfect score:	75
Sequence:	1 MSSSPHVLRNRAOSG 15
Run on:	November 25, 2005, 23:01:59 ; Search time 6.2069 Seconds (without alignments) 232.524 Million cell updates/sec
Scoring table:	BLOSUM62
	Gapop 10.0 , Gapext 0.5
Searched:	283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters:	283416
Maximum DB seq length:	200000000
Minimum DB seq length:	0
Database :	PIR 80:*
	1: pir1:*
	2: pir2:*
	3: pir3:*
	4: pir4:*
Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 1000 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	DB ID	Description
1	75	100.0	2351	1	EZHU	coagulation factor
2	56	74.7	869	2	A25945	coagulation factor
3	56	74.7	2133	2	T42763	coagulation factor
4	50	66.7	440	2	G82426	probable phosphogl
5	43	57.3	2319	2	A47004	coagulation factor
6	42	56.0	355	1	S22181	gamma-1-microglobu
7	40	53.3	133	2	JC7103	endo-1,4-beta-xyla
8	40	53.3	390	2	F83220	hypothetical prote
9	40	53.3	584	2	H95336	probable adenylate
10	40	53.3	616	2	B33586	C4-dicarboxylate t
11	40	53.3	621	2	D96032	C4-dicarboxylate t
12	39	52.0	88	2	C84469	hypothetical prote
13	39	52.0	312	2	B86494	integrase/recombin
14	39	52.0	312	2	F72129	heme A farnesyltra
15	39	52.0	443	2	I38603	hypothetical prote
16	38	50.7	101	2	D70710	DnaJ protein - Syn
17	38	50.7	174	2	S74666	probable membrane
18	38	50.7	186	2	S46093	seed storage prote
19	38	50.7	405	2	JC5175	hypothetical prote
20	38	50.7	567	2	E84504	hypothetical prote
21	38	50.7	2414	2	A54277	transcription adap
22	38	50.7	2441	2	S39161	CREB-binding prote
23	37.5	50.0	698	2	G89787	hypothetical prote
24	38	50.7	133	2	A86283	hypothetical prote
25	37	49.3	138	2	AE1089	Antigen C homolog
26	37	49.3	361	2	AG0335	chorismate synthas
27	37	49.3	383	2	G89902	competence-damage
28	37	49.3	392	2	T51772	acetyl-CoA C-acety
29	37	49.3	650	2	T15972	hypothetical prote
30	37	49.3	1052	2	E71422	hypothetical prote
31	37	49.3	1256	2	T47325	hypothetical prote
32	37	49.3	2275	2	T33123	hypothetical prote
33	36.5	48.7	394	2	B65067	hypothetical prote
34	36.5	48.7	394	2	H85936	probable acyltrans
35	36.5	48.7	394	2	E91091	probable acyltrans
36	36	48.0	62	2	A95281	hypothetical prote
37	36	48.0	153	2	F83097	conserved hypothet
38	36	48.0	227	2	G83948	probable two-compo
39	36	48.0	242	2	T06057	conserved hypothet
40	36	48.0	343	2	AC3603	fructose-bisphosph
41	36	48.0	410	2	T02811	3-methyl-2-oxobuta
42	36	48.0	424	2	B12478	hypothetical prote
43	36	48.0	447	2	D82066	pmbA protein VC253
44	36	48.0	476	2	A71102	conserved hypothet
45	36	48.0	662	2	T44221	probable capsid pr
46	36	48.0	662	2	T44036	DNA excision/repai
47	36	48.0	925	2	T02811	hypothetical prote
48	36	48.0	974	2	T29007	translation elonga
49	36	48.0	1173	2	T25539	hypothetical prote
50	36	48.0	1456	2	T01197	LTR gag/pol polypr
51	35.5	47.3	440	2	E82213	sensor histidine k
52	35.5	47.3	790	2	T05576	hypothetical prote
53	35.5	47.3	137	2	D75337	hypothetical prote
54	35	46.7	175	2	S37756	fanH protein precu
55	35	46.7	178	2	H95020	DNA-3-methyladenin
56	35	46.7	187	2	F97892	DNA-3-methyladenin
57	35	46.7	214	2	G84361	hypothetical prote
58	35	46.7	221	2	G72322	glutaredoxin-relat
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61	35	46.7	269	2	T16910	hypothetical prote
62	35	46.7	309	2	AC3257	integrase/recombin
63	35	46.7	329	2	D95409	probable integrase
64	35	46.7	329	2	D95372	probable integrase
65	35	46.7	344	2	PC4185	hemagglutinin 1 ch
66	35	46.7	345	2	JQ1904	hemagglutinin 1 -
67	35	46.7	345	2	JQ1910	hemagglutinin 1 -
68	35	46.7	345	2	JQ1915	hemagglutinin 1 -
69	35	46.7	345	2	JQ1911	hemagglutinin 1 -
70	35	46.7	345	2	JQ1913	hemagglutinin 1 -
71	35	46.7	345	2	JQ1907	hemagglutinin 1 -
72	35	46.7	345	2	JQ1906	hemagglutinin 1 -
73	35	46.7	345	2	JQ1912	hemagglutinin 1 -
74	35	46.7	345	2	JQ1908	hemagglutinin 1 -
75	35	46.7	345	2	JQ1916	hemagglutinin 1 -
76	35	46.7	345	2	S36080	hemagglutinin 1 -
77	35	46.7	345	2	JQ1914	hemagglutinin 1 - in
78	35	46.7	345	2	JQ1902	hemagglutinin 1 -
79	35	46.7	347	2	JQ1901	hemagglutinin 1 -
80	35	46.7	347	2	JQ1903	hemagglutinin 1 -
81	35	46.7	347	2	JQ1905	hemagglutinin 1 -
82	35	46.7	353	1	JQ1909	hemagglutinin 1 -
83	35	46.7	353	2	HMIVBA	hemagglutinin prec
84	35	46.7	359	2	CS5066	hemagglutinin 1 -
85	35	46.7	378	2	S11738	hemagglutinin prec
86	35	46.7	394	2	F64992	hemagglutinin prec
87	35	46.7	405	2	JQ2147	acetyl-CoA C-acety
88	35	46.7	420	1	S59131	OHP1 protein - mai
89	35	46.7	424	1	E87558	Kan-1 protein - ra
90	35	46.7	488	2	E87236	cytochrome P450 fa
91	35	46.7	496	2	AE0305	ribulose-bisphosph
92	35	46.7	508	2	AE0305	probable sugar tra
93	35	46.7	518	2	T07971	aromatic-L-amino-a
94	35	46.7	521	2	A55066	tyrosine decarboxy
95	35	46.7	523	2	T09615	tyrosine decarboxy
96	35	46.7	531	2	B50066	aromatic-L-amino-a
97	35	46.7	533	2	T07970	tyrosine decarboxy
98	35	46.7	563	2	A22011	hypothetical prote
99	35	46.7	564	2	A22011	aromatic-L-amino-a
100	35	46.7	574	1	HMIVBM	hemagglutinin prec
101	35	46.7	575	2	HMIVBH	hemagglutinin prec
102	35	46.7	575	1	HMIVBH	hemagglutinin prec
			576	2	S01882	hemagglutinin prec
			576	2	S03300	hemagglutinin prec
			578	2	S03299	hemagglutinin prec
			578	2	S03301	hemagglutinin prec

No.	%	%	Len	N	Accession	Description
103	35	46.7	583	1	HMIVBS	hemagglutinin prec
104	35	46.7	583	1	HMIVHO	hemagglutinin prec
105	35	46.7	584	1	HMIVB	hemagglutinin prec
106	35	46.7	585	1	HMIVBJ	hemagglutinin prec
107	35	46.7	607	1	C71367	probable ATP-depen
108	35	46.7	755	2	D75598	photoreceptor - De
109	35	46.7	781	2	AI3448	xanthine dehydroge
110	35	46.7	1078	2	D87647	probable retroelem
111	35	46.7	1102	2	A84480	hypothetical prote
112	35	46.7	1311	2	T33757	probable retroelem
113	35	46.7	1784	2	A49420	tuberous sclerosis
114	35	46.7	1809	2	S57329	tuberous sclerosis
115	35	46.7	2111	2	T15390	hypothetical proce
116	35	46.7	2496	2	A71616	secreted protein P
117	34.5	46.0	391	2	B83155	probable acyl-CoA
118	34.5	46.0	392	2	AE0868	acetyl-CoA C-acety
119	34.5	46.0	396	2	G83326	probable acyl-CoA
120	34.5	46.0	607	1	S58151	hypothetical prote
121	34	45.3	106	2	JC7778	hepatocyte growth
122	34	45.3	209	2	C82656	hypothetical prote
123	34	45.3	251	2	G96006	probable SUR1-like
124	34	45.3	265	2	T40757	conserved hypothet
125	34	45.3	251	2	AF0902	dihydropteroate sy
126	34	45.3	282	2	AP2267	hypothetical prote
127	34	45.3	286	2	T34141	pteridine-dependen
128	34	45.3	297	2	G82763	chorismate synthas
129	34	45.3	306	2	AH3121	conserved hypothet
130	34	45.3	329	2	G99165	hypothetical prote
131	34	45.3	329	1	JC8029	hemagglutinin 1 -
132	34	45.3	347	2	JQ1903	hypothetical prote
133	34	45.3	354	2	D84955	hypothetical prote
134	34	45.3	360	2	AD1929	chorismate synthas
135	34	45.3	361	1	SYEBKR	chorismate synthas
136	34	45.3	361	2	AF0804	chorismate synthas
137	34	45.3	364	2	AD3440	chorismate synthas
138	34	45.3	365	2	B97451	chorismate synthas
139	34	45.3	368	2	JC8029	ornithine carbamoy
140	34	45.3	375	1	XXALAE	acetyl-CoA C-acety
141	34	45.3	393	1	T10476	cell division prot
142	34	45.3	400	2	B84030	stage VI sporulati
143	34	45.3	416	2	B84919	hypothetical prote
144	34	45.3	425	2	JC1417	DNA repair protein
145	34	45.3	460	1	AC1074	probable DNA repai
146	34	45.3	460	2	AD3440	probable ATP-depen
147	34	45.3	460	2	E86138	chaperonin hsp60,
148	34	45.3	460	2	C91297	hypothetical prote
149	34	45.3	465	1	H95369	EgiC ENDO-1,3-1,4-
150	34	45.3	466	1	WMBEHT	capsid protein ICP
151	34	45.3	469	2	B84644	probable protein k
152	34	45.3	496	2	B84030	hypothetical prote
153	34	45.3	500	1	T48812	complement C1 inhi
154	34	45.3	521	2	ITHUC1	hypothetical prote
155	34	45.3	524	2	T27192	hypothetical prote
156	34	45.3	533	2	S46007	chaperonin hsp60,
157	34	45.3	569	2	T49061	beta-fructofuranos
158	34	45.3	583	2	S10035	hypothetical prote
159	34	45.3	597	2	S56680	conserved hypothet
160	34	45.3	597	2	T10034	hydrogenase (EC 1.
161	34	45.3	608	2	D86915	transcription fact
162	34	45.3	618	2	C72405	hypothetical prote
163	34	45.3	620	2	JC4356	NADH2 dehydrogenas
164	34	45.3	675	2	T15273	probable DNA gyras
165	34	45.3	678	2	S53831	DNA topoisomerase
166	34	45.3	697	2	H82035	fatty oxidation co
167	34	45.3	723	2	T03849	Fas-binding protei
168	34	45.3	736	2	T03847	Fas-binding protei
169	34	45.3	740	2	T44142	DR1 protein (impor
170	34	45.3	759	2	T13078	KIAA0992 protein -
171	34	45.3	772	2	T18727	hypothetical prote
172	34	45.3	1008	2	T18724	hypothetical prote
173	34	45.3	1012	2	T25433	hypothetical prote
174	34	45.3	1016	2	B86145	hypothetical prote
175	34	45.3	1025	1	SYEXI	isoleucine-tRNA li
176	34	45.3	1045	1		

No.	%	%	Len	N	Accession	Description
176	34	45.3	1115	2	S64101	PAN2 protein - yea
177	34	45.3	1182	2	T13952	membrane protein P
178	33.5	44.7	1213	2	A54063	TATA-binding prote
179	34	45.3	1237	2	T46609	calcium-activated
180	34	45.3	1237	2	A34598	ecdysone-induced p
181	34	45.3	1298	2	B83175	phosphoribosylform
182	34	45.3	1394	2	B34598	ecdysone-induced p
183	34	45.3	1443	2	S05979	steroid hormone re
184	34	45.3	1678	2	D86481	189.6K hypothetica
185	34	45.3	2700	2	D86450	protein F21H1.2	
186	34	45.3	5762	2	A41819	proline-rich pept1
187	33.5	44.7	389	2	G70769	probable fadA4 pro
188	33.5	44.7	395	2	T51774	acetyl-CoA C-acety
189	33.5	44.7	415	2	T36965	hypothetical prote
190	33	44.0	108	2	T06513	enoyl protein - ga
191	33	44.0	131	2	C75526	hypothetical prote
192	33	44.0	162	2	B86637	acetyl transferase
193	33	44.0	162	2	AG1077	PTS system, fructo
194	33	44.0	162	2	AF1435	PTS system, fructo
195	33	44.0	163	2	S14269	pheromone-binding
196	33	44.0	169	2	T08824	disease resistance
197	33	44.0	186	2	G75474	probable acetyltra
198	33	44.0	186	2	B91133	hypothetical prote
199	33	44.0	186	2	B59978	hypothetical prote
200	33	44.0	186	2	E65105	hypothetical prote
201	33	44.0	191	2	H83719	hypothetical 20.3
202	33	44.0	191	2	C82675	hypothetical prote
203	33	44.0	202	2	S09672	kafirin precursor
204	33	44.0	206	2	H58930	ribosomal protein
205	33	44.0	211	2	AG0917	threonine efflux p
206	33	44.0	220	2	G97376	probable glycohydr
207	33	44.0	227	2	T23358	D-alanine transami
208	33	44.0	234	2	A63555	probable integrase
209	33	44.0	237	2	A64061	hypothetical prote
210	33	44.0	298	2	A39202	hypothetical prote
211	33	44.0	298	2	AB0872	site-specific inte
212	33	44.0	298	2	AF2594	site-specific inte
213	33	44.0	298	2	B85945	site-specific inte
214	33	44.0	299	2	F91099	site-specific reco
215	33	44.0	301	2	AE1109	site-specific reco
216	33	44.0	302	1	B69593	integrase/recombin
217	33	44.0	302	2	D69035	integrase/recombin
218	33	44.0	305	2	A82080	conserved hypothet
219	33	44.0	305	2	T47844	integrase/recombin
220	33	44.0	297	1	A64061	integrase/recombin
221	33	44.0	293	2	D87621	GTP-binding protei
222	33	44.0	275	2	T00503	MJ1232 protein hom
223	33	44.0	269	2	S72259	integrase/recombin
224	33	44.0	267	2	G87079	hypothetical prote
225	33	44.0	242	2	C70438	hypothetical prote
226	33	44.0	237	2	H82681	integrase/recombin
227	33	44.0	234	2	T05303	probable MYB famil
228	33	44.0	227	2	T01944	probable integrase
229	33	44.0	220	2	T26714	hypothetical prote
230	33	44.0	211	2	AC3003	hypothetical prote
231	33	44.0	206	2	T26714	hypothetical prote
232	33	44.0	202	2	F99280	hypothetical prote
233	33	44.0	191	2	P98280	site-specific reco
234	33	44.0	186	2	AC3003	integrase/recombin
235	33	44.0	186	2	T05303	hypothetical prote
236	33	44.0	169	2	P94365	hypothetical prote
237	33	44.0	163	2	PC4365	calcium-binding pr
238	33	44.0	342	2	T28772	plant adhesion mol
239	33	44.0	356	2	T51376	hypothetical prote
240	33	44.0	358	2	T23802	hypothetical prote
241	33	44.0	361	2	SYECKR	chorismate synthas
242	33	44.0	361	2	E91030	chorismate synthas
243	33	44.0	361	2	F85874	chorismate synthas
244	33	44.0	366	2	B81055	chorismate synthas
245	33	44.0	366	2	A81822	chorismate synthas
246	33	44.0	377	1	VHIH79	nucleocapid prote
247	33	44.0	392	2	E83899	thiolase (acetyl-C
248	33	44.0	401	2	A85758	probable oxidoredu

ID	Score	%	Length	N	Accession	Description
249	33	44.0	401	2	B64877	probable membrane
250	33	44.0	401	2	D90861	probable oxidoredu
251	33	44.0	406	2	S55549	serotonin 4 recept
252	33	44.0	406	2	G72244	hypothetical prote
253	33	44.0	407	2	S53900	hypothetical prote
254	33	44.0	429	2	B83257	folylpolyglutamate
255	33	44.0	429	2	G75114	hypothetical prote
256	33	44.0	434	2	A10337	tetrahydrofolylpol
257	33	44.0	437	2	C64113	tetrahydrofolylpol
258	33	44.0	448	2	T15188	hypothetical prote
259	33	44.0	453	2	B69504	seryl-tRNA synthet
260	33	44.0	466	2	A82605	conjugal transfer
261	33	44.0	469	2	AD1926	hypothetical prote
262	33	44.0	477	2	C91034	sucrose-6 phosphat
263	33	44.0	477	2	S52162	sucrose hydrolase
264	33	44.0	482	2	D85878	sucrose hydrolase
265	33	44.0	484	2	G02058	retinoic acid- and
266	33	44.0	502	2	T16695	hypothetical prote
267	33	44.0	502	2	S36494	E2 protein - human
268	33	44.0	503	2	C84595	similar to pEARLI
269	33	44.0	514	2	T49965	hypothetical prote
270	33	44.0	519	2	C71346	hypothetical prote
271	33	44.0	558	2	S68447	probable transcrip
272	33	44.0	583	2	A70723	origin recognition
273	33	44.0	621	2	T15859	probable acyl-coAs
274	33	44.0	656	2	T37941	hypothetical prote
275	33	44.0	657	2	T52460	conserved hypothet
276	33	44.0	673	2	T47905	hypothetical prote
277	33	44.0	690	2	S28222	peroxidase (EC 1.1
278	33	44.0	690	2	S35251	probable membrane
279	33	44.0	694	2	G95314	probable site-spec
280	33	44.0	736	2	D86271	hypothetical prote
281	33	44.0	740	2	T24340	protein P16A14.2 [
282	33	44.0	775	1	VPXRHK	hypothetical prote
283	33	44.0	775	1	VPXRW4	outer layer protei
284	33	44.0	775	1	VPXRWS	outer layer protei
285	33	44.0	775	1	VPXRWF	outer layer protei
286	33	44.0	775	1	VPXRWL	outer layer protei
287	33	44.0	775	1	VPXRWM	outer layer protei
288	33	44.0	798	2	S29815	outer capsid prote
289	33	44.0	797	2	T23927	hypothetical prote
290	33	44.0	798	2	S11210	N-ras upstream pro
291	33	44.0	841	2	T48508	probable unr prote
292	33	44.0	866	2	T06454	beta-adaptin-like
293	33	44.0	889	2	T09055	probable lipoxygen
294	33	44.0	1027	2	H87316	protocadherin 68 -
295	33	44.0	1036	2	S76027	hypothetical prote
296	33	44.0	1048	2	S57155	hypothetical prote
297	33	44.0	1082	2	S64903	NMD5 protein - yea
298	33	44.0	1153	2	S00551	regulatory protein
299	33	44.0	1163	2	G97236	leukocyte surface
300	33	44.0	1216	2	H85023	ATPase involved in
301	33	44.0	1268	2	T31420	hypothetical prote
302	33	44.0	1326	2	T02345	C-terminal domain-
303	33	44.0	1363	2	A53210	secretory phosphol
304	33	44.0	1463	2	T15653	secretory phosphol
305	33	44.0	1465	2	B56395	phospholipase A2 r
306	33	44.0	1791	2	T02345	secretory phosphol
307	33	44.0	1791	2	T33162	hypothetical prote
308	33	44.0	2030	2	A46182	hypothetical prote
309	33	44.0	2180	2	Q2BYU2	hypothetical prote
310	33	44.0	2214	1	A46182	polyprotein - echo
311	32.5	43.3	234	2	AB2960	pyrimidine synthes
312	32.5	43.3	234	2	AB2960	transcription regu
313	32.5	43.3	258	2	D98323	transcription regu
314	32.5	43.3	377	2	T30368	hypothetical prote
315	32.5	43.3	405	2	F71520	probable immediate
316	32.5	43.3	417	2	E82752	hypothetical prote
317	32	42.7	417	2	E98299	cystathionine gamm
318	32	42.7	100	2	AB2984	acetyl-CoA C-acety
319	32	42.7	101	2	T06836	probable acyl-CoA
320	32	42.7	115	2	E82718	30S ribosomal prot
321	32	42.7	120	2	G64304	ribosomal protein

ID	Score	%	Length	N	Accession	Description
322	32	42.7	165	2	T06998	probable H+-transp
323	32	42.7	211	2	E87632	conserved hypothet
324	32	42.7	225	2	S67772	hypothetical prote
325	32	42.7	231	2	AB2164	hypothetical prote
326	32	42.7	245	2	F95420	conserved hypothet
327	32	42.7	253	2	T06113	hypothetical prote
328	32	42.7	259	2	A55274	3-oxo-5alpha-stero
329	32	42.7	259	2	S65744	steroid 5alpha-red
330	32	42.7	276	2	C87296	hydrolase, alpha/b
331	32	42.7	279	2	C29915	hypothetical prote
332	32	42.7	285	2	H85356	ribosomal protein
333	32	42.7	285	2	S70547	hypothetical prote
334	32	42.7	289	2	A81394	sspB protein - Sal
335	32	42.7	303	2	D70503	GTP-binding protei
336	32	42.7	304	2	AH2153	integrase/recombin
337	32	42.7	306	2	AC2442	GTP-binding protei
338	32	42.7	306	1	H85474	conserved hypothet
339	32	42.7	311	2	A29561	probable integrase
340	32	42.7	311	2	B71693	conserved hypothet
341	32	42.7	318	2	JE0325	hypothetical prote
342	32	42.7	322	2	G83728	hypothetical prote
343	32	42.7	334	2	H69873	prostatic spermine
344	32	42.7	335	2	T09887	integrase/recombin
345	32	42.7	341	2	B87571	LIM protein - huma
346	32	42.7	341	2	F97451	phosphoribosylamin
347	32	42.7	345	2	DEBYO	conserved hypothet
348	32	42.7	345	2	AH2669	DNA-binding protei
349	32	42.7	353	2	AC2597	hypothetical prote
350	32	42.7	362	2	C97379	chaperone protein
351	32	42.7	362	2	D82801	dihydroorotase (EC
352	32	42.7	364	1	E84783	molecular chaperon
353	32	42.7	371	2	E95960	conserved hypothet
354	32	42.7	378	2	D91115	hypothetical prote
355	32	42.7	378	2	S22827	probable enzyme pr
356	32	42.7	392	1	XURT	molybdopterin bios
357	32	42.7	395	2	S31196	probable gibberell
358	32	42.7	395	2	S18157	cystathionine beta
359	32	42.7	397	2	T47616	cystathionine beta
360	32	42.7	402	1	WZBFF9	phosphoprotein - N
361	32	42.7	410	2	T04530	acetyl-CoA C-acylt
362	32	42.7	417	2	D85334	hypothetical prote
363	32	42.7	417	2	T42662	hypothetical prote
364	32	42.7	419	1	AH2983	gene 68 protein -
365	32	42.7	419	2	G98299	hypothetical prote
366	32	42.7	424	2	S08084	hypothetical prote
367	32	42.7	428	2	T32021	hypothetical prote
368	32	42.7	428	2	A64092	2-oxoisovalerate d
369	32	42.7	428	2	C33793	2-oxoisovalerate d
370	32	42.7	441	2	F75558	gene IV protein -
371	32	42.7	445	1	C64186	hypothetical prote
372	32	42.7	448	2	G87437	acetyl-CoA C-acety
373	32	42.7	449	2	S58334	hypothetical prote
374	32	42.7	451	2	ADI1284	hypothetical prote
375	32	42.7	451	2	AG1655	pmbA protein - Hae
376	32	42.7	451	1	A70518	hypothetical prote
377	32	42.7	456	2	JS0376	glutamate-5-semial
378	32	42.7	462	2	D28448	menaquinone-specif
379	32	42.7	462	2	T26081	menaquinone-specif
380	32	42.7	463	2	H82865	probable lipU prot
381	32	42.7	463	2	A84588	hypothetical prote
382	32	42.7	465	2	H99931	protein C4G9.8 [i
383	32	42.7	465	2	C69814	hypothetical prote
384	32	42.7	469	2	A84588	conjugal transfer
385	32	42.7	469	2	A84588	dihydrolipoamide d
386	32	42.7	473	2	H99931	probable tyrosine
387	32	42.7	479	2	C69814	benzaldehyde dehyd
388	32	42.7	485	2	A84588	globulin 1 - easte
389	32	42.7	485	2	S18156	hypothetical prote
390	32	42.7	488	2	T26256	spermatogenesis as
391	32	42.7	511	2	T26256	type I site-specif
392	32	42.7	511	2	JC7682	type I restriction
393	32	42.7	514	2	D81952	hypothetical prote
394	32	42.7	517	1	S19243	tyrosinase-related

No.			Len		Accession	Description
395	32	42.7	517	2	T03445	glucose-1-phosphat
396	32	42.7	519	1	YRHUR2	dopachrome isomera
397	32	42.7	520	1	C81424	cytochrome bd oxid
398	32	42.7	523	2	D55066	probable tyrosine
399	32	42.7	523	4	C84699	probable tyrosine
400	32	42.7	535	2	D69679	probable CDC6 prot
401	32	42.7	545	2	C84699	polyketide synthas
402	32	42.7	553	2	T27245	hypothetical protei
403	32	42.7	565	1	VHIVC8	nucleoprotein - in
404	32	42.7	566	1	H84203	phosphate ABC tran
405	32	42.7	568	2	H88904	protein Y57G11C.9
406	32	42.7	569	2	T22516	hypothetical protei
407	32	42.7	580	2	T46024	hypothetical protei
408	32	42.7	586	2	JC6500	hnf-3/forkhead tra
409	32	42.7	592	2	E89772	hypothetical protei
410	32	42.7	593	2	A10850	pathogenicity isla
411	32	42.7	593	2	S70216	sipB protein - Sal
412	32	42.7	593	2	E72803	gp31 protein - Myc
413	32	42.7	617	2	AC0581	penicillin-binding
414	32	42.7	633	2	T19549	hypothetical prote
415	32	42.7	633	2	B31794	mdm-1 protein (clo
416	32	42.7	643	2	T43952	hypothetical prote
417	32	42.7	644	2	T27246	hypothetical prote
418	32	42.7	647	2	T40493	hnf-3/forkhead tra
419	32	42.7	659	2	C70678	probable electron
420	32	42.7	663	2	T06593	arginine decarboxy
421	32	42.7	685	2	T15819	hypothetical prote
422	32	42.7	692	2	C86296	cis/trans isomeras
423	32	42.7	692	2	H83415	AKR1 protein - yea
424	32	42.7	700	2	S48521	hypothetical prote
425	32	42.7	762	2	T23452	hypothetical prote
426	32	42.7	764	2	T23456	hypothetical prote
427	32	42.7	783	2	T48304	hypothetical prote
428	32	42.7	785	2	T14762	UL47h protein - Ma
429	32	42.7	798	2	JQ2205	glucosylceramidase
430	32	42.7	804	2	JC7880	protein F32D8.4 [i
431	32	42.7	808	2	A89201	hypothetical prote
432	32	42.7	831	2	T21621	hypothetical prote
433	32	42.7	870	2	T21659	hypothetical prote
434	32	42.7	878	2	S11177	vacuolar sorting p
435	32	42.7	912	2	S11016	protein W09G3.1a [
436	32	42.7	1011	2	S50293	probable membrane
437	32	42.7	1015	2	E71412	hypothetical prote
438	32	42.7	1025	2	T51016	related to CYC8 pr
439	32	42.7	1040	2	S51899	probable protein k
440	32	42.7	1053	2	H82884	multiple banded an
441	32	42.7	1081	1	T38424	hypothetical prote
442	32	42.7	1103	2	RWHU1B	cell surface glyco
443	32	42.7	1151	2	S30010	probable finger pr
444	32	42.7	1153	2	T13956	timeless protein h
445	32	42.7	1170	2	T18256	probable serine/th
446	32	42.7	1197	2	T18259	serine/threonine p
447	32	42.7	1230	2	G71612	novel serine/threo
448	32	42.7	1230	1	T30871	orsellinic acid sy
449	32	42.7	1233	2	T11158	adenylate cyclase
450	32	42.7	1293	2	S49010	embryonic receptor
451	32	42.7	1309	2	I78875	receptor tyrosine
452	32	42.7	1330	2	B85188	retrotransposon li
453	32	42.7	1333	2	S46224	peroxidasin - frui
454	32	42.7	1474	2	T26589	hypothetical prote
455	32	42.7	1535	2	T26318	hypothetical prote
456	32	42.7	1545	2	JN0786	integrin beta-4 ch
457	32	42.7	1626	2	JC4976	plexin 3 precursor
458	32	42.7	1748	1	E71436	hypothetical prote
459	32	42.7	1872	2	T01526	hypothetical prote
460	32	42.7	2088	2	T06077	splicing factor PR
461	32	42.7	2124	2	B96832	hypothetical prote
462	32	42.7	2352	2	I49729	HD protein - mouse
463	32	42.7	2359	2	GNWVTB	genome polyprotein
464	32	42.7	3119	2	GNWVNE	genome polyprotein
465	32	42.7	3412	1	HSUR1E	histone H1, gonada
466	31.5	42.0	3414	1	T51442	seed maturation-li
467	31.5	42.0	171	1	AB2846	Ca2+/H+ antiporter
	31.5	42.0	355	2		
	31.5	42.0	368	2	AB2846	
	31.5	42.0	368	2	B97623	cpaA protein (AJ00

No.			Len		Accession	Description
468	31.5	42.0	947	2	B86231	hypothetical prote
469	31	41.3	93	2	B83358	hypothetical prote
470	31	41.3	101	2	F86544	hypothetical prote
471	31	41.3	101	2	B72079	hypothetical prote
472	31	41.3	115	2	AD0872	conserved hypothet
473	31	41.3	118	2	G84322	50S ribosomal prot
474	31	41.3	121	2	F72605	50S ribosomal prot
475	31	41.3	121	2	E72651	hypothetical prote
476	31	41.3	130	2	E72605	hypothetical prote
477	31	41.3	130	1	A60224	hypothetical prote
478	31	41.3	132	2	A80751	flagellar protein,
479	31	41.3	135	2	F95368	flagellar protein
480	31	41.3	141	2	F72597	hypothetical prote
481	31	41.3	149	2	B71067	hypothetical prote
482	31	41.3	149	2	AG2279	hypothetical prote
483	31	41.3	151	2	F64026	hypothetical prote
484	31	41.3	151	1	WMVZN1	T3A protein - shee
485	31	41.3	154	2	B29504	hypothetical 18K p
486	31	41.3	159	2	I58352	p16INK4a - mouse
487	31	41.3	161	1	S45846	hypothetical prote
488	31	41.3	161	2	T47743	hypothetical prote
489	31	41.3	167	2	A47207	conserved hypothet
490	31	41.3	175	2	G83642	phycoerythrin beta
491	31	41.3	176	2	A47207	DNA-3-methyladenin
492	31	41.3	176	2	T37815	hypothetical prote
493	31	41.3	177	2	S35252	conserved hypothet
494	31	41.3	177	2	E75637	conserved hypothet
495	31	41.3	183	2	T20391	proline-rich prote
496	31	41.3	186	2	AB1178	glutathione S-tran
497	31	41.3	186	2	T29480	hypothetical prote
498	31	41.3	197	2	F82353	probable chromosom
499	31	41.3	199	2	E90234	hypothetical prote
500	31	41.3	207	2	C95888	conserved hypothet
501	31	41.3	211	2	JC6540	ribosomal protein
502	31	41.3	212	2	T12286	conserved hypothet
503	31	41.3	222	2	E69455	transcription regu
504	31	41.3	222	2	S45026	50S ribosomal prot
505	31	41.3	224	2	H75429	mRNA splicing fact
506	31	41.3	226	2	B83116	hypothetical prote
507	31	41.3	238	2	B87319	bloodstream-specif
508	31	41.3	238	1	T46696	bloodstream-specif
509	31	41.3	239	2	A37416	bloodstream uracil
510	31	41.3	242	2	A43326	dihydrodipicolinat
511	31	41.3	247	2	H42255	hydrogenase-1 cofa
512	31	41.3	242	1	G71334	probable lysophosp
513	31	41.3	282	2	B95858	probable dehydroge
514	31	41.3	287	2	G72634	hypothetical prote
515	31	41.3	288	2	T01247	probable MYB fami1
516	31	41.3	291	2	T13956	nitrilase-related
517	31	41.3	293	2	G75274	probable transcrip
518	31	41.3	293	2	A82967	probable 2-hydroxy
519	31	41.3	296	2	A10043	phosphotransbutyry
520	31	41.3	296	2	I40818	cell division inhi
521	31	41.3	296	2	A64110	eRA GTPase [import
522	31	41.3	296	2	G97059	7,8-dihydropteroat
523	31	41.3	297	2	H91135	7,8-dihydropteroat
524	31	41.3	297	2	C85981	integrase/recombin
525	31	41.3	298	2	F83177	transcription acti
526	31	41.3	300	2	A32837	phosphate butyrylt
527	31	41.3	301	2	C97278	probable smf prote
528	31	41.3	302	2	W92208	hypothetical prote
529	31	41.3	305	2	A38422	insulin-like prote
530	31	41.3	305	2	F71922	hypothetical prote
531	31	41.3	312	2	E64589	acetyl-coenzyme A
532	31	41.3	312	2	E70185	acetyl-CoA carboxy
533	31	41.3	312	2	B70185	mevalonate pyropho
534	31	41.3	313	2	AC0603	asparaginase (EC 3
535	31	41.3	314	2	AC2878	aromatic compounds
536	31	41.3	314	2	A86432	protein TS18.11 [i
537	31	41.3	315	2	AF3270	integrase [importe
538	31	41.3	323	2	T47447	sulfotransferase-1
539	31	41.3	325	2	B97654	ABC transporter ho
540	31	41.3	333	2	T26162	hypothetical prote

ID			Len		Code	Description
541	31	41.3	334	2	A85067	hypothetical prote
542	31	41.3	336	2	JC4102	hypothetical prote
543	31	41.3	337	2	E95423	RepB2 replication
544	31	41.3	339	2	T33477	hypothetical prote
545	31	41.3	340	2	A32433	VSG expression sit
546	31	41.3	347	2	AD1920	ABC phosphate tran
547	31	41.3	347	2	B81243	twitching motility
548	31	41.3	347	2	C82016	probable pilus ret
549	31	41.3	350	2	AF2294	uroporphyrinogen d
550	31	41.3	364	2	G82734	acetylornithine de
551	31	41.3	369	2	T04947	hypothetical prote
552	31	41.3	369	2	A31382	DNA-binding protei
553	31	41.3	378	2	H69280	NADH-dependent fla
554	31	41.3	379	2	G75357	diaminopimelate de
555	31	41.3	381	2	F69666	iron-sulfur cofact
556	31	41.3	381	2	JC4639	silent information
557	31	41.3	383	2	S22611	transcription fact
558	31	41.3	389	2	AD1918	alcohol dehydrogen
559	31	41.3	393	2	F75442	acetyl-CoA acetylt
560	31	41.3	395	2	D97155	stage IV sporulati
561	31	41.3	399	2	B96756	hypothetical prote
562	31	41.3	401	2	B37416	bloodstream-specif
563	31	41.3	401	2	B32433	VSG expression sit
564	31	41.3	402	2	F83422	conserved hypothet
565	31	41.3	410	2	S77661	hypothetical prote
566	31	41.3	416	2	S22611	transcription fact
567	31	41.3	418	2	T45807	translation initia
568	31	41.3	421	2	C82253	folylpolyglutamate
569	31	41.3	422	2	T06388	alpha-galactosidas
570	31	41.3	423	2	T16750	hypothetical prote
571	31	41.3	427	2	I51580	XFKH2 protein - Af
572	31	41.3	427	2	AC1394	human N-acetylgluc
573	31	41.3	427	2	AF1769	weakly human N-ace
574	31	41.3	428	2	A53689	transcription fact
575	31	41.3	429	2	AB0057	hypothetical prote
576	31	41.3	432	2	T31660	threonine synthase
577	31	41.3	436	2	A70923	hypothetical prote
578	31	41.3	436	2	T36104	conserved hypothet
579	31	41.3	439	2	AH2093	dihydroorotase (im
580	31	41.3	440	2	G71522	probable phosphogh
581	31	41.3	445	2	JC2525	UDP-glucose dehydr
582	31	41.3	446	2	A55021	beta-cell E-box tr
583	31	41.3	446	2	D95061	sensor histidine k
584	31	41.3	446	2	H97929	histidine kinase (
585	31	41.3	454	2	B87912	protein B0205.6 (i
586	31	41.3	454	2	A82587	conserved hypothet
587	31	41.3	454	2	S72481	probable transposa
588	31	41.3	458	2	C82682	glutamate-cysteine
589	31	41.3	458	2	S67054	probable membrane
590	31	41.3	461	2	S60253	sel-12 protein - C
591	31	41.3	462	2	AH1566	galactosamine-cont
592	31	41.3	468	2	T33516	hypothetical prote
593	31	41.3	470	2	D87485	glutamyl-tRNA synt
594	31	41.3	473	2	H72744	probable D-lactate
595	31	41.3	474	2	E83392	probable transcrip
596	31	41.3	475	1	UBFPG	tubulin gamma chai
597	31	41.3	478	2	T32476	probable protein-t
598	31	41.3	479	2	T15427	hypothetical prote
599	31	41.3	486	2	S31805	VP5 protein - porc
600	31	41.3	486	2	S15470	NS3 protein - hum
601	31	41.3	490	2	I50708	basic helix-loop-h
602	31	41.3	493	2	S78384	acetyl-CoA carboxy
603	31	41.3	495	2	T31944	hypothetical prote
604	31	41.3	497	2	F83651	hypothetical prote
605	31	41.3	500	2	A11913	apolipoprotein N-a
606	31	41.3	513	2	C75553	hypothetical prote
607	31	41.3	515	2	S52453	ecdysteroid UDP-gl
608	31	41.3	517	2	C83642	hypothetical prote
609	31	41.3	528	2	S24344	glucose transport
610	31	41.3	532	2	D96966	probable sulfate t
611	31	41.3	538	2	D83946	beta-mannanase Man
612	31	41.3	545	2	F83280	probable chemotaxi
613	31	41.3	546	2	B40407	sterol carrier pro
614	31	41.3	551	2	T22121	hypothetical prote
615	31	41.3	573	2	T49610	related to rna bin
616	31	41.3	582	2	C71424	hypothetical prote
617	31	41.3	582	2	T04327	phosphoglucomutase
618	31	41.3	583	2	T04326	phosphoglucomutase
619	31	41.3	583	2	T12574	phosphoglucomutase
620	31	41.3	595	2	H95899	hypothetical prote
621	31	41.3	596	1	I38228	Shb protein - huma
622	31	41.3	601	2	AE3506	sensor protein chv
623	31	41.3	612	2	S52213	hypothetical prote
624	31	41.3	613	2	S27770	hypothetical prote
625	31	41.3	620	2	A81103	probable chaperone
626	31	41.3	620	2	B81118	hypothetical prote
627	31	41.3	621	2	F84638	arginine decarboxy
628	31	41.3	624	2	T15046	nitrogen permease
629	31	41.3	633	1	S44938	arginine permease
630	31	41.3	633	1	ZPCP2	transcription fact
631	31	41.3	633	2	A90713	penicillin-binding
632	31	41.3	633	2	A41311	penicillin-binding
633	31	41.3	667	2	B85563	penicillin-binding
634	31	41.3	642	1	S34416	transcription fact
635	31	41.3	652	2	T20046	hypothetical prote
636	31	41.3	656	2	S55262	UV-endonuclease -
637	31	41.3	657	2	T41546	hypothetical prote
638	31	41.3	666	2	I32648	class A helix-loop
639	31	41.3	691	2	T05432	hypothetical prote
640	31	41.3	667	2	A41111	transcription fact
641	31	41.3	667	2	S89563	hypothetical prote
642	31	41.3	668	2	A46013	coagulation factor
643	31	41.3	670	2	C86432	protein T518.13 (i
644	31	41.3	681	2	S81158	protein C17G10.4c
645	31	41.3	682	2	A42121	transcription fact
646	31	41.3	682	2	C45020	basic-helix-loop-h
647	31	41.3	691	2	S81135	NADH2 dehydrogenas
648	31	41.3	692	2	AD1857	basic-helix-loop-h
649	31	41.3	706	2	S19958	hypothetical prote
650	31	41.3	707	2	A46691	E-box-binding prot
651	31	41.3	719	2	S61046	basic helix-loop-h
652	31	41.3	710	2	T34098	hypothetical prote
653	31	41.3	711	2	S72497	oligopeptide trans
654	31	41.3	714	2	D83897	hypothetical prote
655	31	41.3	719	2	AF2458	AP1 protein - yea
656	31	41.3	733	2	S61046	probable membrane
657	31	41.3	734	2	T48565	hypothetical prote
658	31	41.3	738	2	F96701	hypothetical prote
659	31	41.3	755	2	T19558	hypothetical prote
660	31	41.3	756	2	C84682	hypothetical prote
661	31	41.3	760	2	H84427	hypothetical prote
662	31	41.3	776	2	T51911	heterocyst differe
663	31	41.3	779	2	AC2249	related to protein
664	31	41.3	782	2	T48722	hypothetical prote
665	31	41.3	784	2	T45697	hypothetical prote
666	31	41.3	787	2	A71642	penicillin-binding
667	31	41.3	788	2	JDVLHH	DNA-directed DNA p
668	31	41.3	790	2	E87855	penicillin-binding
669	31	41.3	795	2	T07709	hypothetical prote
670	31	41.3	798	2	A40526	integrin beta-7 ch
671	31	41.3	805	2	S73374	related to protein
672	31	41.3	818	2	T02436	phenylalanine-tRNA
673	31	41.3	865	2	T46651	proline-rich prote
674	31	41.3	867	2	T14777	transcription acti
675	31	41.3	896	2	T51891	hypothetical prote
676	31	41.3	902	2	T41051	beta transducin -
677	31	41.3	907	2	I50404	p50B/p97 (Lyt-10)
678	31	41.3	913	2	T31497	penicillin-binding
679	31	41.3	915	2	S38090	hypothetical prote
680	31	41.3	915	2	T21338	hypothetical prote
681	31	41.3	942	2	S53963	MCS1 protein - yea
682	31	41.3	954	2	T19765	hypothetical prote
683	31	41.3	979	2	JHO592	hypothetical prote
684	31	41.3	979	2	JH0589	glutamate receptor
685	31	41.3	980	2	I57936	glutamate receptor
686	31	41.3	1039	2	C87083	C-term lysyl-tRNA

No.	v1	v2	Len	c	Accession	Description
687	31	41.3	1063	2	T34097	probable protein-t
688	31	41.3	1085	2	S55352	IFH1 protein - yea
689	31	41.3	1091	1	PL0009	complement C3d/Eps
690	31	41.3	1091	1	S50614	regulatory protein
691	31	41.3	1102	2	T28666	protein kinase C-r
692	31	41.3	1112	2	S49432	replicase 126K - o
693	31	41.3	1118	2	A48292	protein kinase C-r
694	31	41.3	1120	2	T14275	mucin, tracheobron
695	31	41.3	1165	2	S62982	myosin-like protei
696	31	41.3	1181	2	T30578	vacuolar protein V
697	31	41.3	1224	2	F96795	myosin IC - slime
698	31	41.3	1237	2	T45070	hypothetical prote
699	31	41.3	1256	2	S14556	protein kinase hom
700	31	41.3	1320	2	H64090	asparagine-rich pr
701	31	41.3	1366	2	C95077	phosphoribosylform
702	31	41.3	1384	2	S78132	probable polyprote
703	31	41.3	1440	2	T29942	DNA-directed RNA p
704	31	41.3	1459	2	S50437	hypothetical prote
705	31	41.3	1526	2	S49763	gingipain R (EC 3.
706	31	41.3	1538	2	E70874	probable ppsB prot
707	31	41.3	1578	2	AD1512	peptidoglycan boun
708	31	41.3	1582	2	T15308	hypothetical prote
709	31	41.3	1582	2	AC1153	adhesin homolog lm
710	31	41.3	1608	1	WMTWGM	183K protein - tob
711	31	41.3	1703	2	S15047	SNF2 protein - yea
712	31	41.3	1728	2	T17466	rifamycin polyketi
713	31	41.3	1763	2	T17465	rifamycin polyketi
714	31	41.3	1888	2	T14273	rifamycin polyketi
715	31	41.3	2028	2	T5022	zinc finger protei
716	31	41.3	2051	2	F96529	1-phosphatidylinos
717	31	41.3	2183	2	T42764	finger protein pML
718	31	41.3	2440	2	S39162	hypothetical prote
719	31	41.3	2562	2	T14266	Tn3 family transpo
720	31	41.3	2672	2	A48126	Xin protein - chic
721	31	41.3	2685	2	T38755	protein F508.34 [i
722	31	41.3	3413	2	T17467	hypothetical prote
723	31	41.3	3839	2	T49799	rifamycin polyketi
724	31	41.3	5069	2	T17464	related to TOM1 pr
725	30.5	40.7	48	1	S27128	rifamycin polyketi
726	30.5	40.7	248	1	HSURLP	histone H1 - sea u
727	30.5	40.7	336	2	A49985	histone H1, Gonada
728	30.5	40.7	339	2	A42259	transaldolase (EC
729	30.5	40.7	371	2	T50159	endo-beta-N-acetyl
730	30.5	40.7	393	2	JN0533	mitochondrial carr
731	30.5	40.7	422	2	T45830	iron(III) ABC tran
732	30.5	40.7	502	2	AB3203	ABC transporter, m
733	30.5	40.7	518	2	B86372	probable zinc fing
734	30.5	40.7	527	2	A84645	probable cytochrom
735	30.5	40.7	554	2	T39979	protein F508.34 [i
736	30.5	40.7	554	2	AH2651	hypothetical prote
737	30.5	40.7	571	2	G97433	probable transcrip
738	30.5	40.7	571	2	S61131	probable membrane
739	30.5	40.7	579	2	T00019	ubiquitin-protein
740	30.5	40.7	601	2	T16944	hypothetical prote
741	30.5	40.7	732	2	T22295	hypothetical prote
742	30.5	40.7	802	2	S43217	protein phosphatas
743	30.5	40.7	809	1	T22296	hypothetical prote
744	30.5	40.7	860	2	T35878	hypothetical prote
745	30.5	40.7	1039	2	T40572	hypothetical prote
746	30.5	40.7	1157	2	T39009	hypothetical prote
747	30.5	40.7	1888	2	T26183	hypothetical prote
748	30.5	40.7	2265	2	AD2055	hypothetical prote
749	30	40.0	56	2	A34326	hypothetical prote
750	30	40.0	62	2	T16276	proctamine - chick
751	30	40.0	77	2	AB3643	hypothetical prote
752	30	40.0	79	2	AI3247	hypothetical prote
753	30	40.0	94	2	AB1439	hypothetical prote
754	30	40.0	97	2	AI1081	a small heat shock
755	30	40.0	97	1	R3EG14	small heat shock p
756	30	40.0	100	2	S78302	ribosomal protein
757	30	40.0	100	2	S76498	wound-induced prot
758	30	40.0	102	2	S36236	ribosomal protein
759	30	40.0	108	2	E75063	hypothetical prote

No.	v1	v2	Len	c	Accession	Description
760	30	40.0	109	2	E72583	hypothetical prote
761	30	40.0	116	2	C86554	sigma regulatory f
762	30	40.0	116	2	E72069	sigma regulatory f
763	30	40.0	121	2	S27105	gene 30.7 protein
764	30	40.0	122	2	H82231	hypothetical prote
765	30	40.0	128	2	T18104	hypothetical prote
766	30	40.0	130	2	T45423	hypothetical prote
767	30	40.0	135	2	D71168	hypothetical prote
768	30	40.0	136	2	T47982	hypothetical prote
769	30	40.0	139	2	D88955	protein K04F1.9 [i
770	30	40.0	148	2	T37717	hypothetical prote
771	30	40.0	149	2	T25963	hypothetical prote
772	30	40.0	150	2	S27613	VP5 homolog - bovi
773	30	40.0	151	2	A47667	rRNA methyltransfe
774	30	40.0	153	2	D39920	probable exported
775	30	40.0	154	2	AG0060	hypothetical prote
776	30	40.0	155	2	B96248	probable cdc2-like
777	30	40.0	157	2	A72457	prolactin, 20K - M
778	30	40.0	160	2	A48975	Thy-1 glycoprotein
779	30	40.0	160	2	S35220	hypothetical prote
780	30	40.0	164	2	S35224	hypothetical prote
781	30	40.0	166	2	S09224	membrane protein -
782	30	40.0	166	2	S09225	membrane protein -
783	30	40.0	167	2	G71548	hypothetical prote
784	30	40.0	167	2	D82122	hypothetical prote
785	30	40.0	172	2	T12202	probable cdc2-like
786	30	40.0	177	2	A28106	prolactin, 20K - M
787	30	40.0	179	2	F69936	hypothetical prote
788	30	40.0	180	2	AD2467	monofunctional cho
789	30	40.0	181	2	A40607	hisP-like nucleoti
790	30	40.0	185	2	F35719	ATP-binding compon
791	30	40.0	185	2	B86104	ATP-binding compon
792	30	40.0	185	2	E91263	hypothetical prote
793	30	40.0	185	2	AG2026	hypothetical prote
794	30	40.0	192	2	G72272	probable transcrip
795	30	40.0	193	2	H83356	amidophosphoribosy
796	30	40.0	194	2	PC1136	hypothetical prote
797	30	40.0	194	2	T47678	prolactin II precu
798	30	40.0	200	2	B32477	hypothetical prote
799	30	40.0	201	2	T07267	endopeptidase Clp
800	30	40.0	204	2	S11460	late L3 23K protei
801	30	40.0	211	2	A64537	conserved hypothet
802	30	40.0	212	2	E82125	hypothetical prote
803	30	40.0	217	2	H90039	very hypothetical
804	30	40.0	217	2	T3781?	hypothetical prote
805	30	40.0	222	2	B95982	germin precursor (
806	30	40.0	224	2	B40391	hypothetical prote
807	30	40.0	225	2	A49941	hypothetical prote
808	30	40.0	228	2	S28019	gene lojap protein
809	30	40.0	233	2	AB2073	hypothetical prote
810	30	40.0	238	2	A52073	splicing factor, a
811	30	40.0	239	2	S49198	GCR 101 protein, a
812	30	40.0	243	2	G81310	probable pyrroline
813	30	40.0	249	2	C84340	ABC transport prot
814	30	40.0	251	2	B82839	3-oxoacyl-[ACP] re
815	30	40.0	252	2	AC1181	hypothetical prote
816	30	40.0	252	2	AD1538	hypothetical prote
817	30	40.0	254	2	F83282	hypothetical prote
818	30	40.0	258	2	B49597	nonstructural prot
819	30	40.0	258	2	A82874	transcription anti
820	30	40.0	261	2	D64075	ureH protein homol
821	30	40.0	263	2	T34526	hypothetical prote
822	30	40.0	264	2	S66151	vent-1 protein - A
823	30	40.0	268	2	T15693	hypothetical prote
824	30	40.0	274	2	S75896	hypothetical prote
825	30	40.0	282	2	AB1029	hypothetical prote
826	30	40.0	283	2	E83053	dihydropteroate sy
827	30	40.0	283	2	A96655	hypothetical prote
828	30	40.0	287	2	A10782	probable transcrip
829	30	40.0	287	2	F81163	integrase/recombin
830	30	40.0	291	2	C81943	probable integrase
831	30	40.0	294	2	D84338	hypothetical prote
832	30	40.0	296	2	C81906	hypothetical prote

ID			Length	Type	Accession	Description
833	30	40.0	296	2	G81111	conserved hypothet
834	30	40.0	296	2	T47598	hypothetical
835	30	40.0	296	2	G84747	AT-hook DNA-bindin
836	30	40.0	301	2	T35805	hypothetical prote
837	30	40.0	302	2	JN0794	phosphate butyrylt
838	30	40.0	303	2	T43913	DNA gyrase chain B
839	30	40.0	303	2	T43912	DNA gyrase chain B
840	30	40.0	303	2	A83958	integrase/recombin
841	30	40.0	304	2	T38957	probable GPR/FUN34
842	30	40.0	304	2	B75595	conserved hypothet
843	30	40.0	307	2	A39999	hypothetical prote
844	30	40.0	308	2	AE3415	integrase [importe
845	30	40.0	310	2	F82979	probable transcrip
846	30	40.0	311	2	C90049	hypothetical prote
847	30	40.0	312	2	T17118	protein kinase cdc
848	30	40.0	313	1	S70839	tidD homolog - Bra
849	30	40.0	314	2	H82115	probable adenine-s
850	30	40.0	316	2	T05591	probable cdc2-like
851	30	40.0	317	2	G82635	methanol dehydroge
852	30	40.0	321	2	D64820	probable asparagin
853	30	40.0	323	2	A82433	fructokinase VCA06
854	30	40.0	323	2	T01103	probable H+-transp
855	30	40.0	323	2	T45531	agaB protein [impo
856	30	40.0	324	1	A41786	mRNA-binding prote
857	30	40.0	325	2	F84740	hypothetical prote
858	30	40.0	325	2	H90204	hypothetical prote
859	30	40.0	326	2	A47493	H+-transporting tw
860	30	40.0	326	2	S50750	dihydrodipicolinat
861	30	40.0	327	2	D84806	hypothetical prote
862	30	40.0	328	2	C69085	DNA repair protein
863	30	40.0	329	2	T47448	sulfotransferase-1
864	30	40.0	330	2	S44160	hypothetical prote
865	30	40.0	330	2	H37386	conserved hypothet
866	30	40.0	332	2	F81743	hypothetical prote
867	30	40.0	333	2	T04656	hypothetical prote
868	30	40.0	333	2	B64380	hypothetical prote
869	30	40.0	335	2	S18143	hypothetical prote
870	30	40.0	337	2	T33957	hypothetical prote
871	30	40.0	337	2	G70741	hypothetical prote
872	30	40.0	340	2	AH0940	probable ABC trans
873	30	40.0	341	2	S60431	hypothetical prote
874	30	40.0	342	2	T46909	hypothetical prote
875	30	40.0	342	2	S57165	hypothetical prote
876	30	40.0	347	2	G86675	carotenoid biosynt
877	30	40.0	348	2	B48435	cysteine proteinas
878	30	40.0	348	2	B82933	type I restriction
879	30	40.0	351	2	A99586	conserved hypothet
880	30	40.0	354	2	T48649	glycerol-3-phospha
881	30	40.0	356	2	A36312	glycerol kinase (E
882	30	40.0	357	1	HLMS37	MHC class I histoc
883	30	40.0	357	2	T37317	probable Ca2+/calm
884	30	40.0	361	2	F82115	chorismate synthas
885	30	40.0	361	2	T01007	mannose-1-phosphat
886	30	40.0	362	2	E83542	hypothetical prote
887	30	40.0	364	2	T47698	mannose-1-phosphat
888	30	40.0	364	2	AD2302	hypothetical prote
889	30	40.0	365	2	I38720	hFcRn - human
890	30	40.0	366	2	C85800	probable cytochrom
891	30	40.0	366	2	G90951	probable cytochrom
892	30	40.0	370	2	F95950	probable ABC trans
893	30	40.0	371	2	H82497	glycerophosphoryl
894	30	40.0	372	1	A55510	chorismate synthas
895	30	40.0	372	2	F86189	hypothetical prote
896	30	40.0	373	2	T21955	hypothetical prote
897	30	40.0	374	2	G70947	hypothetical prote
898	30	40.0	382	2	AI0153	conserved hypothet
899	30	40.0	384	2	AE3189	aminopeptidase Atu
900	30	40.0	385	1	I39498	GTP cyclohydrolase
901	30	40.0	388	2	T43899	DNA gyrase chain B
902	30	40.0	391	1	DEUSO	dihydroorotase (EC
903	30	40.0	391	2	S69192	serine O-acetyltra
904	30	40.0	392	2	T32524	hypothetical prote
905	30	40.0	393	2	G71536	hypothetical prote
906	30	40.0	396	2	S27870	house-keeping prot
907	30	40.0	397	2	S43440	3-oxoacyl-CoA thio
908	30	40.0	398	2	T25719	hypothetical prote
909	30	40.0	398	2	B84888	probable methionin
910	30	40.0	398	2	T43225	pheromone receptor
911	30	40.0	399	2	G96690	unknown protein F2
912	30	40.0	401	2	F87641	methionine-gamma-1
913	30	40.0	401	2	H72765	probable flap endo
914	30	40.0	406	2	A86446	unknown protein [l
915	30	40.0	409	2	T31725	conserved hypothet
916	30	40.0	410	2	AD2844	transforming growt
917	30	40.0	412	2	A36169	conserved hypothet
918	30	40.0	413	2	S73371	hypothetical prote
919	30	40.0	414	2	T43415	probable MADS-box
920	30	40.0	414	2	T49459	hypothetical prote
921	30	40.0	414	2	T21954	hypothetical prote
922	30	40.0	416	2	T31785	hypothetical prote
923	30	40.0	419	2	G87293	ornithine decarbox
924	30	40.0	419	2	T48080	translation releas
925	30	40.0	419	2	A86414	hypothetical prote
926	30	40.0	420	2	T39712	hypothetical prote
927	30	40.0	421	2	S52033	19S proteasome sub
928	30	40.0	422	1	SYECFG	tetrahydrofolylpol
929	30	40.0	422	2	AC0802	dihydrofolate synt
930	30	40.0	424	2	B81936	tetrahydrofolylpol
931	30	40.0	424	2	C81170	folylpolyglutamate
932	30	40.0	426	2	C96804	hypothetical prote
933	30	40.0	427	2	T42516	hypothetical prote
934	30	40.0	428	2	T46046	hypothetical prote
935	30	40.0	428	2	G89982	hypothetical prote
936	30	40.0	435	2	B20096	conserved hypothet
937	30	40.0	435	2	H82501	nicotinate phospho
938	30	40.0	438	2	T47711	hypothetical prote
939	30	40.0	443	2	B70933	hypothetical prote
940	30	40.0	443	2	T48708	hypothetical prote
941	30	40.0	448	2	F83724	hypothetical prote
942	30	40.0	448	2	A48939	Na+-transporting A
943	30	40.0	452	1	H65036	cellobiohydrolase
944	30	40.0	452	2	D91060	CPDdiacylglycerol-
945	30	40.0	454	2	B85905	CPDdiacylglycerol-
946	30	40.0	454	2	A38643	protein kinase (EC
947	30	40.0	457	2	E70081	purine-cytosine pe
948	30	40.0	457	2	T04226	protein kinase (EC
949	30	40.0	459	2	H82080	DNA repair protein
950	30	40.0	459	2	G71431	hypothetical prote
951	30	40.0	460	2	G42246	phosphomannomutase
952	30	40.0	460	2	AI0078	hypothetical prote
953	30	40.0	461	2	T00621	hypothetical prote
954	30	40.0	462	2	B70793	glycerol kinase (E
955	30	40.0	462	2	E69070	hydrogenase expres
956	30	40.0	466	2	G01804	interleukin 3-regu
957	30	40.0	471	2	A84535	Ac-like transposas
958	30	40.0	471	2	S74449	fusca protein homo
959	30	40.0	472	2	T20522	hypothetical homo
960	30	40.0	472	2	I57445	alkaline phosphata
961	30	40.0	476	2	A33387	probable transport
962	30	40.0	477	2	H98235	probable mfs dicar
963	30	40.0	480	2	JC7012	BCL6 homologous zi
964	30	40.0	483	2	T51088	plastid division p
965	30	40.0	484	2	S53641	protein kinase clk
966	30	40.0	485	2	E83775	aldehyde dehydroge
967	30	40.0	485	2	T10792	amidophosphoribosy
968	30	40.0	486	2	S31808	VP5 protein - huma
969	30	40.0	486	2	A89927	elastin binding pr
970	30	40.0	488	2	T33626	hypothetical prote
971	30	40.0	490	2	A38728	ribulose-biphosph
972	30	40.0	491	1	MXRBF	ribulose-biphosph
973	30	40.0	491	2	A49597	nonstructural prot
974	30	40.0	491	2	S31784	nonstructural prot
975	30	40.0	491	2	S31783	VP5 protein - bovi
976	30	40.0	491	2	AC1816	VP5 protein - bovi
977	30	40.0	499	2	A32584	Abd-B protein - fr
978	30	40.0	499	2	H86815	hypothetical prote
	30	40.0	499	2	T89049	hypothetical prote

979	30	40.0	500	2	T40666	acetylglutamate sy
980	30	40.0	500	2	G01646	fusca protein homo
981	30	40.0	506	2	T51702	amidophosphoribosy
982	30	40.0	508	2	S74977	hypothetical prote
983	30	40.0	509	2	E86427	amidophosphoribosy
984	30	40.0	511	2	S52622	hypothetical prote
985	30	40.0	513	2	B84391	coenzyme A transfe
986	30	40.0	514	2	B87711	DNA damage-inducib
987	30	40.0	517	2	JC7623	protein disulfide-
988	30	40.0	518	2	B84967	anthranilate synth
989	30	40.0	518	2	B24723	anthranilate synth
990	30	40.0	518	2	F70831	probable PPE prote
991	30	40.0	522	2	S75491	probable PPE prote
992	30	40.0	532	2	T06087	amidophosphoribosy
993	30	40.0	532	2	JC5412	epidermal growth f
994	30	40.0	533	2	G66140	cobalamin biosynth
995	30	40.0	534	2	T35190	hypothetical prote
996	30	40.0	535	2	B49804	Hsp90 homolog p61
997	30	40.0	540	2	T34187	hypothetical prote
998	30	40.0	548	2	S44654	hypothetical prote
998	30	40.0	552	2	ZK353.1	zK353.1 protein -
999	30	40.0	552	2	AB2361	hypothetical prote
1000	30	40.0	553	2	T02475	hypothetical prote

ALIGNMENTS

RESULT 1

E2HU
coagulation factor VIII precursor [validated] - human
N;Alternate names: antihemophilic factor A; coagulation factor VIIIc; procoagulant compo
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text change 31-Dec-2004
C;Accession: I54318; A23584; A26174; A42548; A43986; S63527; S66445; B42
R;Gitschier, J.; Wood, W.I.
Hum. Mol. Genet. 1, 199-200, 1992
A;Title: Sequence of the exon-containing regions of the human factor VIII gene.
A;Reference number: I54318; MUID:93265012; PMID:1303178
A;Accession: I54318
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1921, 'S', 1923-2351 <RES>
R;Wood, W.I.; Capon, D.J.; Simonsen, C.C.; Eaton, D.L.; Gitschier, J.; Keyt, B.; Seeburg
Nature 312, 330-337, 1984
A;Title: Expression of active human factor VIII from recombinant DNA clones.
A;Reference number: A00525; MUID:85061548; PMID:6438526
A;Accession: A00525
A;Molecule type: mRNA
R;Toole, J.J.; Knopf, J.L.; Wozney, J.M.; Sultzman, L.A.; Buecker, J.L.; Pittman, D.D.;
s, D.N.; Hewick, R.M.
Nature 312, 342-347, 1984
A;Title: Molecular cloning of a cDNA encoding human antihaemophilic factor.
A;Reference number: I58059; MUID:85061550; PMID:6438528
A;Accession: I58059
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-74, 'V', 76-1259, 'E', 1261-2351 <RE2>
R;Truett, M.A.; Blacher, R.; Burke, R.L.; Caput, D.; Chu, C.; Dina, D.; Hartog, K.; Kuo,
B.; Randolph, A.; Urdea, M.S.; Valenzuela, P.; Dahl, H.H.; Favaloro, J.; Hansen, J.; No
DNA 4, 333-349, 1985
A;Title: Characterization of the polypeptide composition of human factor VIII:C and the
A;Reference number: A23584; MUID:86081164; PMID:3955400
A;Accession: A23584
A;Molecule type: mRNA
A;Residues: 1-2351 <TRU>
R;Eaton, D.; Rodriguez, H.; Vehar, G.A.
Biochemistry 25, 505-512, 1986
A;Title: Proteolytic processing of human factor VIII. Correlation of specific cleavages

A;Reference number: A26174; MUID:86159740; PMID:3082357
A;Molecule type: protein
A;Accession: A26174
A;Residues: 20-36, 392-399, 'X', 401-402, 1668-1678, 1709-1722, 'D', 1723-1725, 1741-1755 <EAT>
A;Cross-references: UNIPARC:UPI000012A416; UNIPARC:UPI00001722296; UNIPARC:UPI00001722297; UNIPARC:UPI00001722298;
R;Gitschier, J.; Wood, W.I.; Goralka, T.M.; Wion, K.L.; Chen, E.Y.; Eaton, D.H.; Vehar,
Nature 312, 326-330, 1984
A;Title: Characterization of the human factor VIII gene.
A;Reference number: A56196; MUID:85061547; PMID:6438525
A;Contents: annotation; introns
A;Molecule type: DNA
A;Contents: annotation; introns
A;Note: 329-Cys, 711-Cys, and 2019-Cys were shown to have free sulfhydryls
R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.; Hedner, U.; Ezban, M.
Protein Sci. 4, 740-746, 1995
A;Title: Locations of disulfide bonds and free cysteines in the heavy and light chains o
A;Reference number: A56216; MUID:95338127; PMID:7613471
A;Contents: annotation; disulfide bonds
A;Note: 329-Cys, 711-Cys, and 2019-Cys were shown to have free sulfhydryls
R;Kjalke, M.; Heding, A.; Talbo, G.; Persson, E.; Thomsen, J.; Ezban, M.
Eur. J. Biochem. 234, 773-779, 1995
A;Title: Amino acid residues 721-729 are required for full factor VIII activity.
A;Reference number: S63527; MUID:96163459; PMID:8575434
A;Accession: S63527
A;Molecule type: protein
A;Residues: 733-752, 753-759 <KJA>
A;Cross-references: UNIPARC:UPI00001722A4; UNIPARC:UPI00001722A5
R;Lind, P.; Larsson, K.; Spira, J.; Sydow-Baeckman, M.; Almstedt, A.; Gray, E.; Sandberg
Eur. J. Biochem. 232, 19-27, 1995
A;Title: Novel forms of B-domain-deleted recombinant factor VIII molecules. Construction
A;Reference number: S66445; MUID:96048024; PMID:7556150
A;Accession: S66445
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1668-1685 <LIN>
A;Cross-references: UNIPARC:UPI00001722A6
C;Comment: Factor VIII is activated by factor Xa and thrombin, but prolonged exposure pr
C;Genetics:
A;Gene: GDB:F8C
A;Cross-references: GDB:119124; OMIM:306700
A;Map position: Xq28-Xq28
A;Introns: 48/2; 89/1; 130/1; 201/1; 224/1; 263/1; 337/1; 424/2; 483/3; 513/1; 584/3; 63
C;Function:
A;Description: acts as a cofactor, with calcium and phospholipid, for the factor IXa pro
C;Superfamily: coagulation factors V/VIII; discoidin I amino-terminal homology; ferroxid
C;Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A; pla
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-2351/Product: coagulation factor VIII #status experimental <MAT>
F;20-740/Product: coagulation factor VIII heavy chain #status experimental <ACH>
F;20-356/Domain: A1 <DA1>

A;Reference number: A26174; MUID:86159740; PMID:3082357
A;Molecule type: protein
A;Accession: A26174
A;Residues: 20-36, 371, 392-408, 582-594, 1668-1669, 'X', 1671, 1672-1692, 1693-1708, 1709-17
A;Cross-references: UNIPARC:UPI00001722296; UNIPARC:UPI00001722296; UNIPARC:UPI00001722298; UNIPARC:UPI00001722298;
A;Cross-references: 20-36, 356-371, 392-408, 1668-1669, 'X', 1671, 1672-1692, 1693-1708, 1709-17
A;Molecule type: protein
A;Accession: A42248
A;Reference number: A42248; MUID:92207952; PMID:1554716
A;Title: Identification and functional importance of tyrosine sulfate residues within re
R;Pittman, D.D.; Wang, J.H.; Kaufman, R.J.
Biochemistry 31, 3315-3325, 1992
A;Molecule type: protein
A;Accession: A42548
A;Reference number: A42548; MUID:92207952; PMID:1554716
R;Leyte, A.; van Schindel, H.B.; Niehrs, C.; Huttner, W.B.; Verbeet, M.P.; Mertens, K.;
J. Biol. Chem. 266, 740-746, 1991
A;Title: Sulfation of Tyr(1680) of human blood coagulation factor VIII is essential for
A;Reference number: A56109; MUID:91093266; PMID:1898735
A;Contents: annotation; sulfation
A;Reference number: A43986; MUID:89340500; PMID:2503509
A;Accession: A43986
A;Molecule type: protein
A;Residues: 'X', 517-523, 1953-1960, 'X', 1862-1864, 'X', 1866 <FAY>
A;Cross-references: UNIPARC:UPI00001722A2; UNIPARC:UPI00001722A2; UNIPARC:UPI00001722A3
R;Fay, P.J.; Smudzin, T.M.
J. Biol. Chem. 264, 14005-14010, 1989
A;Title: Intersubunit fluorescence energy transfer in human factor VIII.
A;Reference number: A43986; MUID:89340500; PMID:2503509
A;Accession: A43986
A;Molecule type: protein
A;Note: sequence extracted from NCBI backbone and corrected to correspond with the publi
A;Experimental source: recombinant material from Chinese hamster ovary cells

OM protein - protein search, using sw model

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Run on: November 25, 2005, 22:48:32 ; Search time 36.6207 Seconds
(without alignments)
179.972 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
Sequence: 1 MSSSPHVLRNRAQSG 15

Scoring table: BLOSUM62
   Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Post-processing: Minimum Match 0%
    Maximum Match 100%
    Listing first 1000 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :   A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003aa:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	75	100.0	15	7	ADM75918	Human MHC
2	75	100.0	15	7	ADM75967	Human MHC
3	75	100.0	15	7	ADM75952	Human MHC
4	75	100.0	15	8	ADM75974	Human Fac
5	75	100.0	15	8	ADG06422	Human B-d
6	75	100.0	20	5	ABJ05003	A3 peptid
7	75	100.0	60	10	ABJ04948	A3 domain
8	75	100.0	642	6	ABP60515	Human fac
9	75	100.0	643	6	ABP60514	Human fac
10	75	100.0	684	2	ABP60516	Human fac
11	75	100.0	684	2	AAR73022	Human Fac
12	75	100.0	770	3	AAR74091	Factor-VI
13	75	100.0	790	3	ADP20767	Factor VI
14	75	100.0	1283	3	ADE64594	Recombina
15	75	100.0	1284	1	AAB07205	Human Fac
16	75	100.0	1383	1	AAP50108	Factor-VI
17	75	100.0	1383	2	AAW33227	Procoagul
18	75	100.0	1383	2	AAW33228	Procoagul
19	75	100.0	1402	2	AAW33229	Procoagul
20	75	100.0	1421	8	ADU47620	Human fac
21	75	100.0	1421	8	ADQ37613	Human fac
22	75	100.0	1422	8	ADQ37598	Human Fac
23	75	100.0	1422	8	ADQ37591	Human Fac
24	75	100.0	1423	8	ADU47614	Human fac
25	75	100.0	1424	1	AAP80268	Modified
26	75	100.0	1424	1	AAP91169	Sequence
27	75	100.0	1424	4	AAB48842	Mutant ma
28	75	100.0	1424	8	AAO18622	Human mat
29	75	100.0	1424	9	ADZ65051	Human mat
30	75	100.0	1425	1	AAP80267	Modified
31	75	100.0	1425	8	ADQ37605	Human Fac
32	75	100.0	1425	8	ADQ37590	Human Fac
33	75	100.0	1425	8	ADU47612	Human fac
34	75	100.0	1426	8	ADQ37599	Human Fac
35	75	100.0	1428	8	ADQ37604	Human Fac
36	75	100.0	1428	8	ADQ37589	Human Fac
37	75	100.0	1428	8	ADQ37614	Human Fac
38	75	100.0	1434	8	ADQ37594	Human Fac
39	75	100.0	1434	8	ADQ37609	Human Fac
40	75	100.0	1435	8	ADQ37600	Human Fac
41	75	100.0	1435	8	ADQ37615	Human Fac
42	75	100.0	1437	8	ADQ37593	Human Fac
43	75	100.0	1438	3	AAB01262	B-domain
44	75	100.0	1438	7	ADQ37608	Human Fac
45	75	100.0	1438	7	ADF31316	Variant o
46	75	100.0	1438	7	ADM75988	Modified
47	75	100.0	1438	7	ADM75985	Modified
48	75	100.0	1438	7	ADM75986	Modified
49	75	100.0	1438	7	ADM75983	Wild-type
50	75	100.0	1438	7	ADM75984	Modified
51	75	100.0	1438	7	ADM75987	Modified
52	75	100.0	1440	2	AAR12971	Factor VI
53	75	100.0	1440	8	ADQ37607	Human Fac
54	75	100.0	1440	8	ADQ37592	Human Fac
55	75	100.0	1441	8	ADQ37612	Human Fac
56	75	100.0	1441	8	ADQ37597	Human Fac
57	75	100.0	1442	8	ADQ37616	Human Fac
58	75	100.0	1442	8	ADQ37601	Human Fac
59	75	100.0	1444	8	ADQ37611	Human Fac
60	75	100.0	1444	8	ADQ37596	Human Fac
61	75	100.0	1445	8	ADQ37610	Human Fac
62	75	100.0	1445	9	ABG92540	LE B-doma
63	75	100.0	1445	9	ABG92541	5Arg B-do
64	75	100.0	1447	8	ADQ37595	Human Fac
65	75	100.0	1447	9	AEB96817	5 Arg B-d
66	75	100.0	1447	9	AEB96817	5 Arg B-d
67	75	100.0	1449	8	ADQ37602	Human Fac
68	75	100.0	1449	8	ADQ37617	Human Fac
69	75	100.0	1450	8	ADU47615	Human fac
70	75	100.0	1453	8	ADU47619	Human fac
71	75	100.0	1455	8	ADU47623	Human fac
72	75	100.0	1457	8	ADQ37618	Human Fac
73	75	100.0	1456	8	ADQ37603	Human Fac
74	75	100.0	1456	2	AAW46246	Human fac
75	75	100.0	1457	2	AAW44372	Human fac
76	75	100.0	1457	2	AAY21675	Beta-doma
77	75	100.0	1457	7	ADM98124	HP46/SQ F
78	75	100.0	1457	7	ADM98128	Human B-d
79	75	100.0	1457	8	ADU47569	Human fac
80	75	100.0	1457	8	ADU47618	Human fac
81	75	100.0	1457	8	ADU47622	Human fac
82	75	100.0	1457	8	ADU47623	Human fac
83	75	100.0	1457	8	AAE10833	Human fac
84	75	100.0	1459	4	AAE10827	Human fac
85	75	100.0	1459	4	AAE10832	Human fac
86	75	100.0	1461	8	ADU47616	Human fac
87	75	100.0	1464	8	ADU47624	Human fac
88	75	100.0	1471	2	AAW23414	Amino aci
89	75	100.0	1471	8	ADU47625	Human fac
90	75	100.0	1471	8	ADU47608	Human fac
91	75	100.0	1479	8	ADU47617	Human fac
92	75	100.0	1516	1	AAP80265	Modified
93	75	100.0	1537	8	ADU47610	Human fac
94	75	100.0	1568	8	ADU47621	Human fac
95	75	100.0	1585	8	ADU47607	Human fac
96	75	100.0	1585	8	ADU47613	Human fac
97	75	100.0	1585	8	ADU47613	Human fac

#	75	100.0	Len	N	Accession	Accession	Description
98	75	100.0	1656	8	ADU47611	Adu47611	Human fac
99	75	100.0	1661	2	AAW18670	Aaw18670	Factor VI
100	75	100.0	2096	8	ADQ39369	Adq39369	Human myo
101	75	100.0	2098	8	AAR86863	Aar86863	Factor-VI
102	75	100.0	2271	8	ABM84598	Abm84598	Human dia
103	75	100.0	2332	2	AAR43257	Aar43257	Human Fac
104	75	100.0	2332	2	AAW33224	Aaw33224	Procoagul
105	75	100.0	2332	2	AAW33225	Aaw33225	Procoagul
106	75	100.0	2332	2	AAW33222	Aaw33222	Procoagul
107	75	100.0	2332	2	AAW33226	Aaw33226	Procoagul
108	75	100.0	2332	2	AAW33223	Aaw33223	Procoagul
109	75	100.0	2332	2	AAW44132	Aaw44132	Homo sapi
110	75	100.0	2332	2	AAW53483	Aaw53483	Human fac
111	75	100.0	2332	2	AAY57847	Aay57847	Human fac
112	75	100.0	2332	3	AAY31594	Aay31594	Human fac
113	75	100.0	2332	4	AAE10826	Aae10826	Human mat
114	75	100.0	2332	4	AAB50465	Aab50465	Human fac
115	75	100.0	2332	4	AAB71902	Aab71902	N-termina
116	75	100.0	2332	4	AAE11200	Aae11200	Human fac
117	75	100.0	2332	5	AAU79871	Aau79871	Human fac
118	75	100.0	2332	5	AAU79875	Aau79875	Human fac
119	75	100.0	2332	5	AAU79869	Aau79869	Human fac
120	75	100.0	2332	5	AAU79870	Aau79870	Human fac
121	75	100.0	2332	5	AAU79872	Aau79872	Human fac
122	75	100.0	2332	5	AAU79874	Aau79874	Human fac
123	75	100.0	2332	5	AAU79873	Aau79873	Human fac
124	75	100.0	2332	6	ABP60513	Abp60513	Human fac
125	75	100.0	2332	7	ADM98117	Adm98117	Human mat
126	75	100.0	2332	8	ADF09122	Adf09122	Human fac
127	75	100.0	2332	8	ADL92154	Adl92154	Factor VI
128	75	100.0	2332	8	ADO71703	Ado71703	Amino aci
129	75	100.0	2332	8	ADQ37564	Adq37564	Human ful
130	75	100.0	2332	8	ADR98715	Adr98715	Human fac
131	75	100.0	2332	8	ADR48956	Adr48956	Human fac
132	75	100.0	2332	9	ADW80686	Adw80686	Human fac
133	75	100.0	2332	9	ADW80694	Adw80694	Human fac
134	75	100.0	2332	9	ADW80684	Adw80684	Human fac
135	75	100.0	2332	9	ADW80683	Adw80683	Human fac
136	75	100.0	2332	9	ADW80693	Adw80693	Human fac
137	75	100.0	2332	9	ADW80690	Adw80690	Human fac
138	75	100.0	2332	9	ADW80685	Adw80685	Human fac
139	75	100.0	2332	9	ADW80687	Adw80687	Human fac
140	75	100.0	2332	9	ADW80692	Adw80692	Human fac
141	75	100.0	2332	9	ADW80689	Adw80689	Human fac
142	75	100.0	2332	9	ADW80688	Adw80688	Human fac
143	75	100.0	2332	9	ADW80691	Adw80691	Human fac
144	75	100.0	2332	9	AEA27721	Aea27721	Human Fac
145	75	100.0	2332	9	AEB11788	Aeb11788	Human Fac
146	75	100.0	2332	9	AEB11784	Aeb11784	Human Fac
147	75	100.0	2332	9	AEB11787	Aeb11787	Human Fac
148	75	100.0	2332	9	AEB11778	Aeb11778	Human Fac
149	75	100.0	2332	9	AEB11789	Aeb11789	Human Fac
150	75	100.0	2332	9	AEB11786	Aeb11786	Human Fac
151	75	100.0	2332	9	AEB11785	Aeb11785	Human Fac
152	75	100.0	2332	9	AEB11790	Aeb11790	Human Fac
153	75	100.0	2332	9	AAW11349	Aaw11349	Active Fa
154	75	100.0	2342	2	AAW11422	Aaw11422	Active Fa
155	75	100.0	2343	2	AAW11335	Aaw11335	Active Fa
156	75	100.0	2343	2	AAW11393	Aaw11393	Active Fa
157	75	100.0	2344	2	AAW11432	Aaw11432	Active Fa
158	75	100.0	2344	2	AAW11384	Aaw11384	Active Fa
159	75	100.0	2344	2	AAW11367	Aaw11367	Active Fa
160	75	100.0	2344	2	AAW11410	Aaw11410	Active Fa
161	75	100.0	2344	2	AAW11331	Aaw11331	Active Fa
162	75	100.0	2344	2	AAW11361	Aaw11361	Active Fa
163	75	100.0	2344	2	AAW11370	Aaw11370	Active Fa
164	75	100.0	2345	2	AAW11415	Aaw11415	Active Fa
165	75	100.0	2345	2	AAW11403	Aaw11403	Active Fa
166	75	100.0	2345	2	AAW11348	Aaw11348	Active Fa
167	75	100.0	2345	2	AAW11453	Aaw11453	Active Fa
168	75	100.0	2345	2	AAW11441	Aaw11441	Active Fa
169	75	100.0	2345	2	AAW11383	Aaw11383	Active Fa
170	75	100.0	2345	2	AAW11446	Aaw11446	Active Fa

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171	75	100.0	2346	2	AAW11391	Aaw11391	Active Fa
172	75	100.0	2346	2	AAW11434	Aaw11434	Active Fa
173	75	100.0	2346	2	AAW11351	Aaw11351	Active Fa
174	75	100.0	2346	2	AAW11421	Aaw11421	Active Fa
175	75	100.0	2346	2	AAW11392	Aaw11392	Active Fa
176	75	100.0	2346	2	AAW11452	Aaw11452	Active Fa
177	75	100.0	2346	2	AAW11431	Aaw11431	Active Fa
178	75	100.0	2346	2	AAW11356	Aaw11356	Active Fa
179	75	100.0	2346	2	AAW11360	Aaw11360	Active Fa
180	75	100.0	2347	2	AAW11411	Aaw11411	Active Fa
181	75	100.0	2347	2	AAW11379	Aaw11379	Active Fa
182	75	100.0	2347	2	AAW11340	Aaw11340	Active Fa
183	75	100.0	2347	2	AAW11369	Aaw11369	Active Fa
184	75	100.0	2348	2	AAW11402	Aaw11402	Active Fa
185	75	100.0	2348	2	AAW11341	Aaw11341	Active Fa
186	75	100.0	2348	2	AAW11436	Aaw11436	Active Fa
187	75	100.0	2348	2	AAW11390	Aaw11390	Active Fa
188	75	100.0	2348	2	AAW11409	Aaw11409	Active Fa
189	75	100.0	2348	2	AAW11378	Aaw11378	Active Fa
190	75	100.0	2348	2	AAW11449	Aaw11449	Active Fa
191	75	100.0	2348	2	AAW11386	Aaw11386	Active Fa
192	75	100.0	2348	2	AAW11448	Aaw11448	Active Fa
193	75	100.0	2348	2	AAW11395	Aaw11395	Active Fa
194	75	100.0	2348	2	AAW11414	Aaw11414	Active Fa
195	75	100.0	2348	2	AAW11365	Aaw11365	Active Fa
196	75	100.0	2349	2	AAW11444	Aaw11444	Active Fa
197	75	100.0	2349	2	AAW11366	Aaw11366	Active Fa
198	75	100.0	2349	2	AAW11428	Aaw11428	Active Fa
199	75	100.0	2349	2	AAW11424	Aaw11424	Active Fa
200	75	100.0	2349	2	AAW11443	Aaw11443	Active Fa
201	75	100.0	2349	2	AAW11346	Aaw11346	Active Fa
202	75	100.0	2350	2	AAW11375	Aaw11375	Active Fa
203	75	100.0	2350	2	AAW11339	Aaw11339	Active Fa
204	75	100.0	2350	2	AAW11380	Aaw11380	Active Fa
205	75	100.0	2350	2	AAW11358	Aaw11358	Active Fa
206	75	100.0	2350	2	AAW11359	Aaw11359	Active Fa
207	75	100.0	2350	2	AAW11376	Aaw11376	Active Fa
208	75	100.0	2350	2	AAW11430	Aaw11430	Active Fa
209	75	100.0	2350	2	AAW11443	Aaw11443	Active Fa
210	75	100.0	2350	2	AAW11339	Aaw11339	Active Fa
211	75	100.0	2350	2	AAW11358	Aaw11358	Active Fa
212	75	100.0	2350	2	AAW11373	Aaw11373	Active Fa
213	75	100.0	2350	2	AAW11355	Aaw11355	Active Fa
214	75	100.0	2350	2	AAW11376	Aaw11376	Active Fa
215	75	100.0	2350	2	AAW11405	Aaw11405	Active Fa
216	75	100.0	2350	2	AAW11413	Aaw11413	Active Fa
217	75	100.0	2351	1	AAW11405	Aaw11405	Human fac
218	75	100.0	2351	1	AAP60741	Aap60741	Human fac
219	75	100.0	2351	1	AAP81113	Aap81113	Factor VI
220	75	100.0	2351	1	AAP80659	Aap80659	Sequence
221	75	100.0	2351	2	AAP80659	Aap80659	Sequence
222	75	100.0	2351	2	AAS55352	Aas55352	Sequence
223	75	100.0	2351	2	AAR78223	Aar78223	Human Fac
224	75	100.0	2351	2	AAW00465	Aaw00465	Factor-VI
225	75	100.0	2351	2	AAW11371	Aaw11371	Active Fa
226	75	100.0	2351	2	AAW11408	Aaw11408	Active Fa
227	75	100.0	2351	2	AAW11427	Aaw11427	Active Fa
228	75	100.0	2351	2	AAW11347	Aaw11347	Active Fa
229	75	100.0	2351	2	AAW11445	Aaw11445	Active Fa
230	75	100.0	2351	2	AAW11404	Aaw11404	Active Fa
231	75	100.0	2351	2	AAW11416	Aaw11416	Active Fa
232	75	100.0	2351	2	AAW11398	Aaw11398	Active Fa
233	75	100.0	2351	2	AAW11332	Aaw11332	Active Fa
234	75	100.0	2351	2	AAW11399	Aaw11399	Active Fa
235	75	100.0	2351	2	AAW11425	Aaw11425	Active Fa
236	75	100.0	2351	2	AAW11343	Aaw11343	Active Fa
237	75	100.0	2351	2	AAW11371	Aaw11371	Active Fa
238	75	100.0	2351	2	AAW11437	Aaw11437	Native Fa
239	75	100.0	2351	2	AAW11329	Aaw11329	Active Fa
240	75	100.0	2351	2	AAW11377	Aaw11377	Active Fa
241	75	100.0	2351	2	AAW11396	Aaw11396	Active Fa
242	75	100.0	2351	2	AAW11435	Aaw11435	Active Fa
243	75	100.0	2351	2	AAW11387	Aaw11387	Active Fa

No.	%1	%2	Len	n	Accession	Name	Description
244	75	100.0	2351	2	AAW11419	Aaw11419	Active Fa
245	75	100.0	2351	2	AAW11454	Aaw11454	Active Fa
246	75	100.0	2351	2	AAW13496	Aaw13496	Factor VI
247	75	100.0	2351	2	AAW10591	Aaw10591	Factor VI
248	75	100.0	2351	2	AAW10590	Aaw10590	Factor VI
249	75	100.0	2351	2	AAW10592	Aaw10592	Factor VI
250	75	100.0	2351	2	AAW46245	Aaw46245	Human fac
251	75	100.0	2351	2	AAW44373	Aaw44373	Human Fac
252	75	100.0	2351	2	AAY21676	Aay21676	Factor VI
253	75	100.0	2351	2	AAY52537	Aay52537	Human ful
254	75	100.0	2351	4	AAB48843	Aab48843	Human fac
255	75	100.0	2351	5	AAO18620	Aao18620	Human fac
256	75	100.0	2351	6	ABR55853	Abr55853	Human Fac
257	75	100.0	2351	6	ABB99528	Abb99528	Amino aci
258	75	100.0	2351	7	ADK48888	Adk48888	Wild type
259	75	100.0	2351	7	ADK48895	Adk48895	Wild type
260	75	100.0	2351	7	ADK48899	Adk48899	Wild type
261	75	100.0	2351	7	ADK48898	Adk48898	Wild type
262	75	100.0	2351	7	ADK48896	Adk48896	Wild type
263	75	100.0	2351	7	ADK48894	Adk48894	Wild type
264	75	100.0	2351	7	ADK48893	Adk48893	Wild type
265	75	100.0	2351	7	ADK48897	Adk48897	Wild type
266	75	100.0	2351	8	ADM98133	Adm98133	Full-leng
267	75	100.0	2351	8	ADN49702	Adn49702	Human Fac
268	75	100.0	2351	8	ADQ39371	Adq39371	Human myo
269	75	100.0	2351	8	ADR98714	Adr98714	Human nat
270	75	100.0	2351	8	ADT92117	Adt92117	Human fac
271	75	100.0	2351	8	ADU47567	Adu47567	Human fac
272	75	100.0	2351	8	ADU74378	Adu74378	Human fac
273	75	100.0	2351	9	ADZ65063	Adz65063	Human fac
274	75	100.0	2351	9	ADZ65059	Adz65059	Human fac
275	75	100.0	2351	9	ADZ65061	Adz65061	Human fac
276	75	100.0	2351	9	ADZ65048	Adz65048	Human fac
277	75	100.0	2351	9	ADZ65057	Adz65057	Human fac
278	75	100.0	2351	9	AEA89878	Aea89878	Factor VI
279	75	100.0	2351	2	AAW11337	Aaw11337	Active Fa
280	75	100.0	2351	2	AAW11353	Aaw11353	Active Fa
281	75	100.0	2351	2	AAW11364	Aaw11364	Active Fa
282	75	100.0	2351	2	AAW11406	Aaw11406	Active Fa
283	75	100.0	2351	2	AAW11330	Aaw11330	Active Fa
284	75	100.0	2351	2	AAW11389	Aaw11389	Active Fa
285	75	100.0	2351	2	AAW11333	Aaw11333	Active Fa
286	75	100.0	2351	2	AAW11345	Aaw11345	Active Fa
287	75	100.0	2351	2	AAW11407	Aaw11407	Active Fa
288	75	100.0	2351	2	AAW11429	Aaw11429	Active Fa
289	75	100.0	2351	2	AAW11418	Aaw11418	Active Fa
290	75	100.0	2351	2	AAW11433	Aaw11433	Active Fa
291	75	100.0	2351	2	AAW11357	Aaw11357	Active Fa
292	75	100.0	2351	2	AAW11372	Aaw11372	Active Fa
293	75	100.0	2351	2	AAW11400	Aaw11400	Active Fa
294	75	100.0	2351	2	AAW11447	Aaw11447	Active Fa
295	75	100.0	2351	2	AAW11344	Aaw11344	Active Fa
296	75	100.0	2351	2	AAW11368	Aaw11368	Active Fa
297	75	100.0	2351	2	AAW11394	Aaw11394	Active Fa
298	75	100.0	2351	2	AAW11350	Aaw11350	Active Fa
299	75	100.0	2351	2	AAW11354	Aaw11354	Active Fa
300	75	100.0	2351	2	AAW11363	Aaw11363	Active Fa
301	75	100.0	2351	2	AAW11382	Aaw11382	Active Fa
302	75	100.0	2351	2	AAW11397	Aaw11397	Active Fa
303	75	100.0	2351	2	AAW11374	Aaw11374	Active Fa
304	75	100.0	2351	2	AAW11412	Aaw11412	Active Fa
305	75	100.0	2351	2	AAW11439	Aaw11439	Active Fa
306	75	100.0	2351	2	AAW11381	Aaw11381	Active Fa
307	75	100.0	2351	2	AAW11385	Aaw11385	Active Fa
308	75	100.0	2351	2	AAW11417	Aaw11417	Active Fa
309	75	100.0	2351	2	AAW11334	Aaw11334	Active Fa
310	75	100.0	2351	2	AAW11336	Aaw11336	Active Fa
311	75	100.0	2351	2	AAW11426	Aaw11426	Active Fa
312	75	100.0	2351	2	AAW11342	Aaw11342	Active Fa
313	75	100.0	2352	2	AAW11388	Aaw11388	Active Fa
314	75	100.0	2352	2	AAW11423	Aaw11423	Active Fa
315	75	100.0	2352	2	AAW11438	Aaw11438	Active Fa
316	75	100.0	2352	2	AAW11442	Aaw11442	Active Fa
317	75	100.0	2352	2	AAW11450	Aaw11450	Active Fa
318	75	100.0	2352	2	AAW11451	Aaw11451	Active Fa
319	73	97.3	2351	1	AAP70448	Aap70448	Human fac
320	70	93.3	1014	7	AAP71139	Aap71139	Facor VII
321	70	93.3	1438	1	ADM75989	Adm75989	Modified
322	70	93.3	2332	1	AAP71726	Aap71726	Facor VII
323	70	93.3	2332	1	AAP71728	Aap71728	Facor VII
324	70	93.3	2332	1	AAP71729	Aap71729	Facor VII
325	70	93.3	2332	1	AAP71727	Aap71727	Facor VII
326	70	93.3	1431	4	AAW11461	Aaw11461	Active Fa
327	69	92.0	1431	4	AAB67960	Aab67960	Active Fa
328	69	92.0	2343	3	AAW80989	Aaw80989	Canine fa
329	69	92.0	2343	3	AAY57846	Aay57846	Canine fa
330	69	92.0	2351	1	AAP50319	Aap50319	Human ant
331	65	86.7	13	7	ADM75497	Adm75497	Potential
332	64.5	86.0	2352	2	AAW11459	Aaw11459	Active Fa
333	64.5	86.0	2352	2	AAW11456	Aaw11456	Active Fa
334	64.5	86.0	2352	2	AAW11458	Aaw11458	Active Fa
335	64.5	86.0	2352	2	AAW11463	Aaw11463	Active Fa
336	64.5	86.0	2352	2	AAW11464	Aaw11464	Active Fa
337	64	85.3	13	7	ADM75762	Adm75762	Potential
338	63	84.0	2351	2	AAW11468	Aaw11468	Active Fa
339	63	84.0	2351	2	AAW11472	Aaw11472	Active Fa
340	63	84.0	2351	2	AAW11471	Aaw11471	Active Fa
341	60	80.0	2345	2	AAW11466	Aaw11466	Active Fa
342	59.5	79.3	320	3	AAB07207	Aab07207	Human Fac
343	58	77.3	13	7	ADM74968	Adm74968	Potential
344	57	76.0	41	2	AAP50313	Aap50313	Thrombin
345	56	74.7	16	2	AAR49460	Aar49460	Factor VI
346	56	74.7	13	7	ADM75232	Adm75232	Potential
347	56	74.7	73	3	AAB07206	Aab07206	Thrombin
348	56	74.7	211	1	AAP50091	Aap50091	Truncated
349	56	74.7	211	1	AAB07203	Aab07203	Human Fac
350	56	74.7	868	2	AAR51143	Aar51143	Porcine F
351	56	74.7	1443	4	AAW44137	Aaw44137	Homo sapi
352	56	74.7	1443	2	AAY31598	Aay31598	Porcine f
353	56	74.7	1443	4	AAB50469	Aab50469	Porcine f
354	56	74.7	1467	7	AAB11207	Aab11207	Modified
355	56	74.7	1467	7	ADD01038	Add01038	Recombina
356	56	74.7	1467	7	ADM98132	Adm98132	HP63/OL F
357	56	74.7	1467	7	ADM98130	Adm98130	HP47/OL F
358	56	74.7	1467	7	ADM98126	Adm98126	HP44/OL F
359	56	74.7	1467	7	ADM98115	Adm98115	Porcine f
360	56	74.7	1467	8	ADO71702	Ado71702	Amino aci
361	56	74.7	2114	8	ADR48955	Adr48955	Porcine f
362	56	74.7	2114	9	AEA27722	Aea27722	Pig Facto
363	56	74.7	2114	3	AAY57849	Aay57849	Pig Facto
364	56	74.7	2115	3	AAW44133	Aaw44133	Sus scrof
365	56	74.7	2133	2	AAY31597	Aay31597	Porcine f
366	56	74.7	2133	7	AAB50468	Aab50468	Porcine f
367	56	74.7	2133	4	AAE11203	Aae11203	Porcine f
368	56	74.7	2133	7	ADK48890	Adk48890	Wild type
369	56	74.7	2133	7	ADM98113	Adm98113	Porcine f
370	56	74.7	2347	2	AAW11467	Aaw11467	Active Fa
371	55	74.7	2349	2	AAW11470	Aaw11470	Active Fa
372	53.5	71.3	2350	2	AAW11460	Aaw11460	Active Fa
373	52	69.3	2349	2	AAW11457	Aaw11457	Active Fa
374	51.5	68.7	2350	2	AAW11455	Aaw11455	Active Fa
375	47.5	63.3	2348	2	ADM75233	Adm75233	Potential
376	47	62.7	14	8	ABM79481	Abm79481	Human Fac
377	45	60.0	13	7	ADM74967	Adm74967	Potential
378	45	60.0	20	5	ABJ05002	Abj05002	A3 peptid
379	45	60.0	116	6	ABU64637	Abu64637	Propionib
380	45	60.0	116	5	ABM61156	Abm61156	Propionib
381	44	58.7	2347	2	AAW11469	Aaw11469	Active Fa
382	43	57.3	1561	5	ADH48884	Adh48884	Propionib
383	43	57.3	2304	3	NOV70	Nov70	pro
384	43	57.3	2319	2	AAY57848	Aay57848	Active Fa
385	43	57.3	2319	2	AAW44135	Aaw44135	Mus muscu
386	43	57.3	2319	2	AAW53485	Aaw53485	Murine fa
387	43	57.3	2319	2	AAY31596	Aay31596	Murine fa
388	43	57.3	2319	2	AAB50467	Aab50467	Mouse fac
389	43	57.3	2319	4	AAE11202	Aae11202	Murine Fa

					Accession	Description
390	43	57.3	2319	7	ABK48892	Adk48892 Wild type
391	43	57.3	2319	7	ADM98119	Adm98119 Murine fa
392	40	53.3	13	7	ADM75761	Adm75761 Potential
393	40	53.3	33	1	AAP50318	Aap50318 Peptide e
394	40	53.3	290	7	ABM87660	Abm87660 Rice abio
395	40	53.3	356	5	ABG91502	Abg91502 Purine/py
396	39	53.3	391	7	ABO79668	Abo79668 Pseudomon
397	39	52.0	61	5	ABP09722	Abp09722 Human ORF
398	39	52.0	83	4	AAU53907	Aau53907 Propionib
399	39	52.0	83	7	ABM50426	Abm50426 Propionib
400	39	52.0	84	8	ADX750097	Adx750097 Plant ful
401	39	52.0	86	5	ADK36508	Adk36508 Novel hum
402	39	52.0	131	2	AAY34624	Aay34624 Chlamydia
403	39	52.0	161	9	ADY65916	Ady65916 S. manson
404	39	52.0	190	4	AAU43382	Aau43382 Propionib
405	39	52.0	190	6	ABM39901	Abm39901 Propionib
406	39	52.0	208	0	ABR41655	Abr41655 Human DIT
407	39	52.0	251	4	AAB70067	Aab70067 Human sec
408	39	52.0	251	8	ABG65506	Abg65506 Human alb
409	39	52.0	251	8	ADL78773	Adl78773 Albumin f
410	39	52.0	314	4	AAB70085	Aab70085 Human sec
411	39	52.0	324	4	ABG06360	Abg06360 Novel hum
412	39	52.0	405	4	ABG13587	Abg13587 Novel hum
413	39	52.0	473	6	ABR58058	Abr58058 Human bee
414	39	52.0	473	6	ABR43181	Abr43181 Human REM
415	39	52.0	562	4	ABG21605	Abg21605 Novel hum
416	39	52.0	744	4	AAB94796	Aab94796 Human pro
417	39	52.0	1095	4	ABG21602	Abg21602 Novel hum
418	39	52.0	1095	4	ABG21823	Abg21823 Novel hum
419	39	52.0	1261	8	ADO63071	Ado63071 Transcrip
420	39	52.0	1454	7	ADJ69522	Adj69522 Human hea
421	39	52.0	1493	5	ABU03484	Abu03484 Angiogene
422	39	52.0	1498	6	ABP98044	Abp98044 Human str
423	38.5	51.3	64	3	AAP78434	Aap78434 N. gonorr
424	38.5	51.3	314	3	AAB32517	Aab32517 S. lavend
425	38.5	51.3	611	7	ADE10289	Ade10289 S. lavend
426	38	50.7	47	3	AAB51422	Aab51422 Human sec
427	38	50.7	73	7	ADM26040	Adm26040 Hyperther
428	38	50.7	137	9	ADV95417	Adv95417 Yeast ubi
429	38	50.7	145	9	ADV95419	Adv95419 Yeast ubi
430	38	50.7	151	7	ABO79467	Abo79467 Pseudomon
431	38	50.7	186	3	AAY82472	Aay82472 Yeast APG
432	38	50.7	223	8	ADY09987	Ady09987 Plant ful
433	38	50.7	264	8	ADX88933	Adx88933 Plant ful
434	38	50.7	302	4	AAB82483	Aab82483 Cotton tr
435	38	50.7	315	8	ADY10878	Ady10878 Plant ful
436	38	50.7	433	2	ABR83623	Abr83623 APG12-GFP
437	38	50.7	514	6	AAE30854	Aae30854 p300 prot
438	38	50.7	800	2	ABP70130	Abp70130 Transcrip
439	38	50.7	983	4	ABB70130	Abb70130 Drosophil
440	38	50.7	2414	2	AAR84882	Aar84882 Transcrip
441	38	50.7	2414	5	AAW40057	Aaw40057 Cellular
442	38	50.7	2414	5	ABB06340	Abb06340 Human p30
443	38	50.7	2414	6	ABU03968	Abu03968 Human exp
444	38	50.7	2414	6	ABU03980	Abu03980 Human exp
445	38	50.7	2414	6	ABU03975	Abu03975 Human exp
446	38	50.7	2414	6	ABU03978	Abu03978 Human exp
447	38	50.7	2414	6	ABU03976	Abu03976 Human exp
448	38	50.7	2441	2	AAR79054	Aar79054 CREB bind
449	38	50.7	2441	2	AAW40058	Aaw40058 Cellular
450	38	50.7	2441	4	AAY94252	Aay94252 Mouse nuc
451	38	50.7	2441	4	ABB44555	Abb44555 Mouse wou
452	38	50.7	2441	6	ABU03977	Abu03977 Human exp
453	38	50.7	2441	8	ADF90352	Adf90352 Mouse CRE
454	38	50.7	2441	8	ADR87292	Adr87292 Mouse CRE
455	37.5	50.0	388	6	ABU45477	Abu45477 Protein e
456	37.5	50.0	698	6	ABU16049	Abu16049 Protein e
457	37.5	50.0	698	8	ABM72008	Abm72008 Staphyloc
458	37	49.3	67	0	AAW77529	Aaw77529 Staphyloc
459	37	49.3	73	4	AAU44285	Aau44285 Propionib
460	37	49.3	73	6	ABM40804	Abm40804 Propionib
461	37	49.3	77	4	AAU46907	Aau46907 Propionib
462	37	49.3	77	6	ABM43426	Abm43426 Propionib

					Accession	Description
463	37	49.3	80	4	ABG02132	Abg02132 Novel hum
464	37	49.3	97	8	ADN21282	Adn21282 Bacterial
465	37	49.3	102	7	ADE72560	Ade72560 Human end
466	37	49.3	135	8	ADY22596	Ady22596 Plant ful
467	37	49.3	138	5	ABB49084	Abb49084 Listeria
468	37	49.3	195	7	ABM73600	Abm73600 DNA clone
469	37	49.3	197	3	AAG61029	Aag61029 Arabidops
470	37	49.3	245	5	ABB58522	Abb58522 Drosophil
471	37	49.3	343	8	ADX71828	Adx71828 Plant ful
472	37	49.3	353	8	ADN24650	Adn24650 Bacterial
473	37	49.3	361	7	ABU50323	Abu50323 Protein e
474	37	49.3	362	8	ADN25827	Adn25827 Bacterial
475	37	49.3	366	8	ABU21594	Abu21594 Protein e
476	37	49.3	368	8	ADN21892	Adn21892 Bacterial
477	37	49.3	369	6	ABU22711	Abu22711 Protein e
478	37	49.3	371	6	ABU19941	Abu19941 Protein e
479	37	49.3	375	6	ABU16859	Abu16859 Protein e
480	37	49.3	383	5	ABM73109	Abm73109 Staphyloc
481	37	49.3	390	7	ABO73986	Abo73986 Pseudomon
482	37	49.3	392	4	AAY21893	Aay21893 PHA beta-
483	37	49.3	416	7	ABU19669	Abu19669 Protein e
484	37	49.3	443	4	AAB92694	Aab92694 Human pro
485	37	49.3	445	7	ABU20061	Abu20061 Protein e
486	37	49.3	451	8	ADE54766	Ade54766 Rat Prote
487	37	49.3	451	8	ADF46968	Adf46968 Rat endom
488	37	49.3	459	8	ADX90946	Adx90946 Plant ful
489	37	49.3	481	7	ADY09710	Ady09710 Plant ful
490	37	49.3	514	8	ABS59278	Abs59278 Drosophil
491	37	49.3	516	8	AEB28047	Aeb28047 Enterobac
492	37	49.3	525	4	ABB70056	Abb70056 Human gen
493	37	49.3	534	7	ADJ69571	Adj69571 Human hea
494	37	49.3	534	8	ADM57332	Adm57332 Recombina
495	37	49.3	553	7	ABO69238	Abo69238 Pseudomon
496	37	49.3	595	7	ADI14038	Adi14038 Human src
497	37	49.3	595	8	ADX06363	Adx06363 Cyclin-de
498	37	49.3	595	9	ADJ75374	Adj75374 Marker ge
499	37	49.3	602	4	ADZ70496	Adz70496 Human pro
500	37	49.3	602	4	AAB94639	Aab94639 Human pro
501	37	49.3	638	7	ADI15051	Adi15051 Human pro
502	37	49.3	638	8	ABM81297	Abm81297 Tumour-as
503	37	49.3	666	3	ABB98191	Abb98191 Gab2 amin
504	37	49.3	676	9	ABM81296	Abm81296 Tumour-as
505	37	49.3	853	4	ADY15196	Ady15196 PRO polyp
506	37	49.3	853	4	AAB95413	Aab95413 Human pro
507	37	49.3	862	4	ABP97756	Abp97756 Amino aci
508	37	49.3	875	2	ABP97752	Abp97752 Amino aci
509	37	49.3	886	4	ABB64308	Abb64308 Drosophil
510	37	49.3	974	4	ADS42617	Ads42617 Bacterial
511	37	49.3	1037	4	AAB93585	Aab93585 Bacterial
512	37	49.3	1038	7	ADF42720	Adf42720 Human MP1
513	37	49.3	1038	7	ADJ69037	Adj69037 Human hea
514	37	49.3	1038	8	ADJ75373	Adj75373 Marker ge
515	37	49.3	1038	8	ADI14093	Adi14093 Human pro
516	37	49.3	1038	8	ADL83112	Adl83112 Human sar
517	37	49.3	1038	9	ADR40195	Adr40195 Human met
518	37	49.3	1038	9	ADX06361	Adx06361 Cyclin-de
519	37	49.3	1038	9	ADY20444	Ady20444 PRO polyp
520	37	49.3	1256	8	ADO61875	Ado61875 Transcrip
521	37	48.7	90	7	ADF59535	Adf59535 Human pol
522	36.5	48.7	102	4	AAM06596	Aam06596 Protein e
523	36.5	48.7	392	6	ABU28000	Abu28000 Protein e
524	36.5	48.7	392	7	ABU31880	Abu31880 Protein e
525	36.5	48.7	393	4	ABO65420	Abo65420 Klebsiell
526	36.5	48.7	394	4	AAU34687	Aau34687 E. coli c
527	36.5	48.7	394	8	ABU28743	Abu28743 Protein e
528	36	48.7	394	7	ADS45108	Ads45108 Bacterial
529	36	48.7	13	7	ADM75496	Adm75496 Bacterial
530	36	48.7	55	7	ABP64580	Abp64580 Human ORF
531	36	48.0	70	4	AAU59407	Aau59407 Potential
532	36	48.0	70	6	ABM55926	Abm55926 Propionib
533	36	48.0	91	7	AAG33515	Aag33515 Arabidops
534	36	48.0	94	5	ABP10022	Abp10022 Human ORF
535	36	48.0	96	3	AAG33829	Aag33829 Arabidops

ID			Len	n	Accession	Description
*536	36	48.0	130	7	ADD27459	Human adi
^537	36	48.0	131	7	ADD26770	Human adi
538	36	48.0	158	8	ADY10193	Plant ful
539	36	48.0	167	3	AAG33647	Arabidops
540	36	48.0	168	8	ADY13891	Plant ful
541	36	48.0	188	8	ADY07159	Plant ful
542	36	48.0	196	4	ADY04601	Plant ful
543	36	48.0	211	7	ABO73289	Pseudomon
544	36	48.0	226	3	AAG33964	Arabidops
545	36	48.0	242	7	ABO75465	Pseudomon
546	36	48.0	242	7	ADS28281	Bacterial
547	36	48.0	270	8	ADI67231	Lactobaci
548	36	48.0	297	7	ABB68227	Drosophil
549	36	48.0	352	7	ABO70195	Pseudomon
550	36	48.0	353	6	ABU23250	Protein e
551	36	48.0	388	8	ADS30490	Bacterial
552	36	48.0	398	8	AAG50427	Arabidops
553	36	48.0	398	3	AAG05034	Arabidops
554	36	48.0	398	9	ABM93460	M. xanthu
555	36	48.0	398	9	AEB27175	Pinus rad
556	36	48.0	402	6	ADA32994	Actinetoba
557	36	48.0	403	7	ABO65895	Klebsiell
558	36	48.0	413	8	ADL05522	M. catarr
559	36	48.0	414	7	ABM86166	Rice ablo
560	36	48.0	469	5	ABP65741	Bifidobac
561	36	48.0	556	7	ABO76086	Pseudomon
562	36	48.0	682	6	ABU22671	Protein e
563	36	48.0	775	8	ADS23728	Bacterial
564	36	48.0	1173	8	ADN22372	Bacterial
565	36	48.0	1364	4	AAG70912	S cerevis
566	36	48.0	1425	4	ABG23344	Novel hum
567	36	48.0	1510	4	ABB61116	Drosophil
568	36	48.0	19938	6	ABP76678	Streptomy
569	35.5	47.3	465	2	AAW60723	36K antig
570	35.5	47.3	2346	2	AAW11462	Active Fa
571	36	46.7	50	5	ABP01227	Human ORF
572	36	46.7	56	8	ABO56633	Human gen
573	36	46.7	59	4	AAU62446	Propionib
574	36	46.7	59	6	ABM58965	Propionib
575	36	46.7	60	4	AAU42633	Propionib
576	36	46.7	60	6	ABM39152	Propionib
577	36	46.7	63	8	ADG22708	Cyanophag
578	36	46.7	66	6	ADA33042	Acinetoba
579	36	46.7	93	6	AAM92700	Human dig
580	36	46.7	95	4	AAU55023	Propionib
581	36	46.7	95	6	ABM51542	Propionib
582	36	46.7	110	4	AAM78951	Human pro
583	36	46.7	110	9	AAB95703	Human pro
584	36	46.7	110	9	ADY16369	PRO polyp
585	36	46.7	121	6	AAO00937	Human sec
586	36	46.7	125	4	ABB97804	Human pol
587	36	46.7	128	4	AAO01183	Human pol
588	36	46.7	130	6	ABO04879	Human col
589	36	46.7	134	4	AAM24090	Equine ES
590	36	46.7	139	5	AAW56427	Amino end
591	36	46.7	139	5	ABP07045	Human ORF
592	36	46.7	139	2	ABP02250	Human ORF
593	36	46.7	143	4	AAM79935	Human pro
594	36	46.7	143	8	ADR66467	Human pro
595	36	46.7	146	3	ADR66125	Human pro
596	36	46.7	146	5	AAY75280	Neisseria
597	36	46.7	147	4	ABO76191	Pseudomon
598	35	46.7	167	4	AAU57010	Propionib
599	35	46.7	167	6	ABM53529	Propionib
600	35	46.7	178	6	ABU00518	S. Pneumo
601	35	46.7	180	3	AAB32785	Eucalyptu
602	35	46.7	187	8	ADK48286	Streptoco
603	35	46.7	190	9	ADR96197	Streptoco
604	35	46.7	202	5	ABB90006	Novel S.
605	35	46.7	225	4	AEA60067	Human pol
606	35	46.7	266	4	AAG91257	C glutami
607	35	46.7	270	8	ADX67924	Plant ful
608	35	46.7	270	8	ADX67924	Plant ful

ID			Len	n	Accession	Description	Name
609	35	46.7	271	4	AAB80635	Environme	Aab80635 Environme
610	35	46.7	289	4	ABG20652	Novel hum	Abg20652 Novel hum
611	35	46.7	295	4	AAB93831	Human pro	Aab93831 Human pro
612	35	46.7	295	7	ADC31815	Human nov	Adc31815 Human nov
613	35	46.7	297	6	ABU38953	Protein e	Abu38953 Protein e
614	35	46.7	300	9	ABM92672	M. xanthu	Abm92672 M. xanthu
615	35	46.7	315	4	AAU46880	Propionib	Aau46880 Propionib
616	35	46.7	315	6	ABM43399	Propionib	Abm43399 Propionib
617	35	46.7	326	7	ADC31814	Human nov	Adc31814 Human nov
618	35	46.7	345	2	AAR51856	Influenza	Aar51856 Influenza
619	35	46.7	345	2	AAR51857	Influenza	Aar51857 Influenza
620	35	46.7	345	2	AAR51853	Influenza	Aar51853 Influenza
621	35	46.7	345	2	AAR51854	Influenza	Aar51854 Influenza
622	35	46.7	345	2	AAR51855	Influenza	Aar51855 Influenza
623	35	46.7	345	2	AAR51851	Influenza	Aar51851 Influenza
624	35	46.7	345	2	AAR51849	Influenza	Aar51849 Influenza
625	35	46.7	345	2	AAR51852	Influenza	Aar51852 Influenza
626	35	46.7	345	2	AAR51850	Influenza	Aar51850 Influenza
627	35	46.7	345	2	AAR51848	Influenza	Aar51848 Influenza
628	35	46.7	346	8	ADM19055	Influenza	Adm19055 Influenza
629	35	46.7	347	6	ADM36115	Protein e	Adm36115 Protein e
630	35	46.7	347	8	AAR51846	Influenza	Aar51846 Influenza
631	35	46.7	347	2	AAR51847	Influenza	Aar51847 Influenza
632	35	46.7	349	9	ADW18198	E_grandis	Adw18198 E_grandis
633	35	46.7	349	9	ADW18624	Eucalyptu	Adw18624 Eucalyptu
634	35	46.7	353	9	ADW38201	Rat iPLA2	Adw38201 Rat iPLA2
635	35	46.7	354	7	ADB65176	Human pro	Adb65176 Human pro
636	35	46.7	361	6	ABU36115	Klebsiell	Abu36115 Klebsiell
637	35	46.7	361	4	ABU31873	Protein e	Abu31873 Protein e
638	35	46.7	374	3	AAG13431	Arabidops	Aag13431 Arabidops
639	35	46.7	374	8	ADT55756	Plant pol	Adt55756 Plant pol
640	35	46.7	375	5	AAE18954	Human cel	Aae18954 Human cel
641	35	46.7	377	7	ABO66029	Klebsiell	Abo66029 Klebsiell
642	35	46.7	378	3	AAG13430	Arabidops	Aag13430 Arabidops
643	35	46.7	388	8	ABP40106	Staphyloc	Abp40106 Staphyloc
644	35	46.7	388	8	ADS05035	Staphyloc	Ads05035 Staphyloc
645	35	46.7	391	8	ABU18760	Protein e	Abu18760 Protein e
646	35	46.7	391	8	ADS26505	Bacterial	Ads26505 Bacterial
647	35	46.7	391	8	ADS26876	Bacterial	Ads26876 Bacterial
648	35	46.7	391	8	ADS27247	Bacterial	Ads27247 Bacterial
649	35	46.7	391	8	ADN25419	Bacterial	Adn25419 Bacterial
650	35	46.7	393	8	ABU17952	Protein e	Abu17952 Protein e
651	35	46.7	393	8	ADS27583	Bacterial	Ads27583 Bacterial
652	35	46.7	394	8	ADN18249	Bacterial	Adn18249 Bacterial
653	35	46.7	410	8	ADS23037	Bacterial	Ads23037 Bacterial
654	35	46.7	426	8	ADO62574	Transcrip	Ado62574 Transcrip
655	35	46.7	435	8	ADX93126	Plant ful	Adx93126 Plant ful
656	35	46.7	457	7	ABU31743	Protein e	Abu31743 Protein e
657	35	46.7	460	4	AAB94655	Drosophil	Aab94655 Drosophil
658	35	46.7	462	4	ABB61367	Klebsiell	Abb61367 Klebsiell
659	35	46.7	463	7	ABO62517	Pseudomon	Abo62517 Pseudomon
660	35	46.7	484	7	ABO71037	Pseudomon	Abo71037 Pseudomon
661	35	46.7	521	6	ADA55103	Bacterial	Ada55103 Bacterial
662	35	46.7	583	2	ADY27591	Hemagglut	Ady27591 Hemagglut
663	35	46.7	583	2	ADY27585	Hemagglut	Ady27585 Hemagglut
664	35	46.7	584	2	AAE23121	Hemagglut	Aae23121 Hemagglut
665	35	46.7	584	9	ADY27587	Hemagglut	Ady27587 Hemagglut
666	35	46.7	584	9	ADY27589	Hemagglut	Ady27589 Hemagglut
667	35	46.7	585	2	ADY27597	Hemagglut	Ady27597 Hemagglut
668	35	46.7	585	2	AAW01671	Influenza	Aaw01671 Influenza
669	35	46.7	585	2	AAW75443	Influenza	Aaw75443 Influenza
670	35	46.7	585	9	AAE04953	Influenza	Aae04953 Influenza
671	35	46.7	585	9	ADY27593	Hemagglut	Ady27593 Hemagglut
672	35	46.7	585	9	ADY27595	Hemagglut	Ady27595 Hemagglut
673	35	46.7	586	2	AAW01675	Influenza	Aaw01675 Influenza
674	35	46.7	586	2	AAW75447	Influenza	Aaw75447 Influenza
675	35	46.7	586	4	AAW01674	Influenza	Aaw01674 Influenza
676	35	46.7	586	4	AAW75446	Influenza	Aaw75446 Influenza
677	35	46.7	592	2	AAE04956	Influenza	Aae04956 Influenza
678	35	46.7	592	2	AAE08658	Novel pro	Aae08658 Novel pro
679	35	46.7	607	2	ABU48470	Protein e	Abu48470 Protein e
680	35	46.7	607	6	ADE55072	Human Pro	Ade55072 Human Pro
681	35	46.7	610	7	ADX67924	Plant ful	Adx67924 Plant ful

No.	%	%	Len	#	Accession	Accession	Description
682	35	46.7	614	8	ADQ65458	Adq65458	Novel hum
683	35	46.7	632	8	ADN27275	Adn27275	Bacterial
684	35	46.7	648	7	ADF75109	Adf75109	A_gossypi
685	35	46.7	708	7	ABB61380	Abb61380	Drosophil
686	35	46.7	716	8	ADV89014	Adv89014	Streptoco
687	35	46.7	716	8	ADV80267	Adv80267	Streptoco
688	35	46.7	726	4	AAG66716	Aag66716	Human tra
689	35	46.7	726	8	AAO30813	Aao30813	Human cel
690	35	46.7	746	8	ADV82390	Adv82390	Streptoco
691	35	46.7	849	8	AAY70968	Aay70968	Human Ras
692	35	46.7	913	5	ABP66191	Abp66191	Bifidobac
693	35	46.7	940	3	AAY53040	Aay53040	Human sec
694	35	46.7	940	8	ADK70539	Adk70539	Respirato
695	35	46.7	980	8	ABM82887	Abm82887	Human dia
696	35	46.7	993	9	AEA17265	Aea17265	Mouse gua
697	35	46.7	1011	7	ADE63009	Ade63009	Human Pro
698	35	46.7	1011	7	ADE63013	Ade63013	Human Pro
699	35	46.7	1021	7	ABO78659	Abo78659	Pseudomon
700	35	46.7	1078	8	ADS28006	Ads28006	Bacterial
701	35	46.7	1205	6	ABM67325	Abm67325	Photorhab
702	35	46.7	1311	8	ADN23286	Adn23286	Bacterial
703	35	46.7	1596	8	ABB70845	Abb70845	Drosophil
704	35	46.7	1596	8	ADS96464	Ads96464	Drosophil
705	35	46.7	1723	8	ADO10059	Ado10059	Novel hum
706	35	46.7	1784	2	AAR77223	Aar77223	Tuberous
707	34.5	46.7	1807	7	ADB85512	Adb85512	Human GTG
708	34.5	46.7	1807	7	ADC16723	Adc16723	Human mod
709	34.5	46.7	1807	8	ADQ18517	Adq18517	Human sof
710	34.5	46.7	1809	7	ADE55015	Ade55015	Rat Prote
711	34.5	46.7	1809	7	ADE55009	Ade55009	Rat Prote
712	34.5	46.7	1809	7	ADE55006	Ade55006	Rat Prote
713	34.5	46.7	1809	7	ADE55012	Ade55012	Rat Prote
714	34.5	46.7	1883	8	ADM87281	Adm87281	Human pro
715	34.5	46.7	1904	6	ABR57428	Abr57428	Human NOV
716	34.5	46.7	1911	8	ABU11041	Abu11041	Human pro
717	35	46.7	2496	3	AAB18222	Aab18222	Plasmodiu
718	35	46.7	392	3	ABU48286	Abu48286	Protein e
719	34.5	46.7	393	7	ABO71502	Abo71502	Pseudomon
720	34.5	46.7	402	4	AAU38284	Aau38284	Salmonell
721	34.5	46.7	406	4	ABB69665	Abb69665	Drosophil
722	34.5	46.7	426	4	AAU34208	Aau34208	Staphyloc
723	34.5	46.7	664	7	ABO82604	Abo82604	Pseudomon
724	34.5	46.7	705	4	AAU36870	Aau36870	Staphyloc
725	34.5	46.0	778	6	ADA55561	Ada55561	Human pro
726	34.5	46.0	819	7	ADB64601	Adb64601	Human pro
727	34	45.3	53	5	AAU60249	Aau60249	Propionib
728	34	45.3	53	6	ABM56768	Abm56768	Propionib
729	34	45.3	56	3	AAG02000	Aag02000	Human sec
730	34	45.3	56	4	AAU50827	Aau50827	Propionib
731	34	45.3	56	6	ABM47346	Abm47346	Propionib
732	34	45.3	58	6	ABU24493	Abu24493	Protein e
733	34	45.3	62	6	AAU64471	Aau64471	Propionib
734	34	45.3	62	5	ABP27396	Abp27396	Streptoco
735	34	45.3	71	6	ABM60990	Abm60990	Propionib
736	34	45.3	71	4	AAG74968	Aag74968	Human col
737	34	45.3	75	4	AAU51209	Aau51209	Propionib
738	34	45.3	75	6	ABM47728	Abm47728	Propionib
739	34	45.3	85	4	AAB58503	Aab58503	Lung canc
740	34	45.3	85	6	AAG78985	Aag78985	Human nuc
741	34	45.3	85	7	ADM80579	Adm80579	Nuclear p
742	34	45.3	96	6	ADN02549	Adn02549	imup-2 pr
743	34	45.3	96	2	AAY00330	Aay00330	Human sec
744	34	45.3	96	7	ADG90360	Adg90360	Novel hum
745	34	45.3	96	9	ADG90179	Adg90179	Human pro
746	34	45.3	100	6	ADY25519	Ady25519	Novel hum
747	34	45.3	100	6	ADA54553	Ada54553	Human pro
748	34	45.3	102	3	AAG27084	Aag27084	Zea mays
749	34	45.3	104	3	AAG27083	Aag27083	Zea mays
750	34	45.3	106	4	AAG78984	Aag78984	Human nuc
751	34	45.3	106	7	ADM80577	Adm80577	Nuclear p
752	34	45.3	106	7	ADM80580	Adm80580	Nuclear p
753	34	45.3	106	4	ADM80576	Adm80576	Nuclear p
754	34	45.3	106	7	ADN02547	Adn02547	imup-1 pr

No.	%	%	Len	#	Accession	Accession	Description
755	34	45.3	106	7	ADN02550	Adn02550	imup-2 pr
756	34	45.3	106	4	ADN02546	Adn02546	imup-1 pr
757	34	45.3	113	3	AAY76584	Aay76584	Human ova
758	34	45.3	131	3	AAY75282	Aay75282	Neisseria
759	34	45.3	134	7	ADE65222	Ade65222	Human pro
760	34	45.3	137	5	ABP00207	Abp00207	Human ORF
761	34	45.3	138	4	AAU54545	Aau54545	Propionib
762	34	45.3	138	6	ABM51064	Abm51064	Propionib
763	34	45.3	140	4	AAG27082	Aag27082	Zea mays
764	34	45.3	147	4	AAU58708	Aau58708	Propionib
765	34	45.3	147	6	ABM55227	Abm55227	Propionib
766	34	45.3	149	4	AAU57064	Aau57064	Propionib
767	34	45.3	149	6	ABM53583	Abm53583	Propionib
768	34	45.3	154	4	ABG01354	Abg01354	Novel hum
769	34	45.3	160	4	AAU55910	Aau55910	Propionib
770	34	45.3	162	7	ABM52429	Abm52429	Propionib
771	34	45.3	165	7	ADB64678	Adb64678	Human pro
772	34	45.3	166	3	ADP81190	Adp81190	Protein o
773	34	45.3	172	4	AAB44111	Aab44111	Human can
774	34	45.3	172	6	AAU61439	Aau61439	Propionib
775	34	45.3	172	6	ABM57958	Abm57958	Propionib
776	34	45.3	185	4	AAU54247	Aau54247	Propionib
777	34	45.3	185	6	ABM50766	Abm50766	Propionib
778	34	45.3	192	6	ABU57266	Abu57266	Human pol
779	34	45.3	213	4	AAU18651	Aau18651	Renal and
780	34	45.3	213	6	AAU17093	Aau17093	Novel sig
781	34	45.3	214	4	ADP93801	Adp93801	Human nov
782	34	45.3	215	7	ABB60881	Abb60881	Drosophil
783	34	45.3	231	4	ADB60881	Adb60881	Human pro
784	34	45.3	231	9	ABU65411	Abu65411	Human pro
785	34	45.3	231	9	ADY18931	Ady18931	Human PRO
786	34	45.3	231	9	AEA23724	Aea23724	PRO polyp
787	34	45.3	233	6	ABU19678	Abu19678	Protein e
788	34	45.3	235	7	ADV26409	Adv26409	Human STA
789	34	45.3	237	5	AAU69525	Aau69525	Human G p
790	34	45.3	237	8	AAU66845	Aau66845	Propionib
791	34	45.3	238	6	ABM63364	Abm63364	Bacterial
792	34	45.3	242	7	ADG14978	Adg14978	Human pol
793	34	45.3	246	4	ADY05015	Ady05015	Human SEC
794	34	45.3	256	4	ADG10467	Adg10467	Plant ful
795	34	45.3	262	7	ABU47719	Abu47719	Protein e
796	34	45.3	273	8	ABI10467	Abi10467	Protein e
797	34	45.3	275	8	ABI18131	Abi18131	Protein e
798	34	45.3	275	7	ABU18803	Abu18803	Protein e
799	34	45.3	279	6	ABM89255	Abm89255	Human olf
800	34	45.3	282	8	AAU24766	Aau24766	Human olf
801	34	45.3	282	4	AAU95768	Aau95768	Human olf
802	34	45.3	296	6	AAU85386	Aau85386	G-coupled
803	34	45.3	299	4	ADC85873	Adc85873	Human GPC
804	34	45.3	299	6	ADG83510	Adg83510	Human GPC
805	34	45.3	305	5	ADI19287	Adi19287	Human G p
806	34	45.3	305	4	ADP07851	Adp07851	Human sec
807	34	45.3	305	8	AAG72194	Aag72194	Human olf
808	34	45.3	305	5	ADD13489	Add13489	C. glutam
809	34	45.3	305	7	AAB43417	Aab43417	Protein e
810	34	45.3	310	7	ABU27701	Abu27701	Protein e
811	34	45.3	310	4	AAW72022	Aaw72022	Influenza
812	34	45.3	317	4	AAR51845	Aar51845	HSV-2 str
813	34	45.3	325	4	ABM89255	Abm89255	Rice ablo
814	34	45.3	327	7	ADB11608	Adb11608	Allococo
815	34	45.3	345	2	ABU47621	Abu47621	Human pro
816	34	45.3	347	2	AAU38361	Aau38361	Salmonell
817	34	45.3	351	2	ABU39783	Abu39783	Protein e
818	34	45.3	351	7	AAG65592	Aag65592	Protein e
819	34	45.3	357	7	AAG45295	Aag45295	Arabidops
820	34	45.3	361	4	ADY07252	Ady07252	Plant ful
821	34	45.3	362	6	ABG01765	Abg01765	Novel hum
822	34	45.3	363	8	ADS23256	Ads23256	Bacterial
823	34	45.3	365	6			
824	34	45.3	365	3			
825	34	45.3	365	8			
826	34	45.3	366	4			
827	34	45.3	371	8			

ID			Len	N	Accession	Accession	Description
828	34	45.3	375	2	AAR43664	Aar43664	Ornithine
829	34	45.3	375	2	AAR43663	Aar43663	Ornithine
830	34	45.3	376	3	AAG06591	Aag06591	Arabidops
831	34	45.3	376	3	AAG45294	Aag45294	Arabidops
832	34	45.3	376	9	AEA266993	Aea266993	Stress to
833	34	45.3	381	8	ADS129986	Ads129986	TRICH-9.
834	34	45.3	385	3	AAG45293	Aag45293	Arabidops
835	34	45.3	385	3	AAG48864	Aag48864	Arabidops
836	34	45.3	385	3	AAG06080	Aag06080	Arabidops
837	34	45.3	385	7	ABP70161	Abp70161	Amino aci
838	34	45.3	385	9	ABM86299	Abm86299	Rice abio
839	34	45.3	385	9	ADY20020	Ady20020	PRO polyp
840	34	45.3	386	9	ADP99175	Adp99175	Human tra
841	34	45.3	388	8	AAG06590	Aag06590	Arabidops
842	34	45.3	392	3	AAG48863	Aag48863	Arabidops
843	34	45.3	392	3	AAG06079	Aag06079	Arabidops
844	34	45.3	392	8	ADN21728	Adn21728	Bacterial
845	34	45.3	392	8	ADN24482	Adn24482	Bacterial
846	34	45.3	393	1	AAP94156	Aap94156	Beta-keto
847	34	45.3	393	8	AAR10680	Aar10680	Thiolase
848	34	45.3	393	2	AAR32191	Aar32191	Sequence
849	34	45.3	393	5	AAB71980	Aab71980	Ralstonia
850	34	45.3	393	6	ABU10966	Abu10966	Poly3-hyd
851	34	45.3	393	6	ABU22707	Abu22707	Protein e
852	34	45.3	393	8	ADP83240	Adp83240	PhaA with
853	34	45.3	394	8	ADS42848	Ads42848	Bacterial
854	34	45.3	395	8	ABU21267	Abu21267	Protein e
855	34	45.3	395	6	ABU41778	Abu41778	Protein e
856	34	45.3	398	8	ABU39983	Abu39983	Protein e
857	34	45.3	402	9	ABM97411	Abm97411	M. xanthu
858	34	45.3	408	7	ABM85834	Abm85834	Mouse pro
859	34	45.3	409	8	ADX66970	Adx66970	Plant ful
860	34	45.3	417	3	AAB25777	Aab25777	Human sec
861	34	45.3	417	5	AAU74633	Aau74633	Human sec
862	34	45.3	417	8	ADP19164	Adp19164	Human sec
863	34	45.3	425	8	ADX73005	Adx73005	Plant ful
864	34	45.3	426	8	ABU19824	Abu19824	Protein e
865	34	45.3	433	3	AAB42762	Aab42762	Human ORF
866	34	45.3	434	8	ADY22775	Ady22775	Plant ful
867	34	45.3	434	8	ADY09019	Ady09019	Plant ful
868	34	45.3	436	6	ABU22367	Abu22367	Protein e
869	34	45.3	437	8	ADY11647	Ady11647	Plant ful
870	34	45.3	443	3	ADN26405	Adn26405	Bacterial
871	34	45.3	446	3	AAY99670	Aay99670	Human GTP
872	34	45.3	446	4	AAM93739	Aam93739	Human pol
873	34	45.3	446	4	AAM39368	Aam39368	Human pol
874	34	45.3	446	8	ABU52686	Abu52686	Human sig
875	34	45.3	446	8	ADL31676	Adl31676	Human pro
876	34	45.3	446	6	ABM82158	Abm82158	Tumour-as
877	34	45.3	451	6	ABU21586	Abu21586	Protein e
878	34	45.3	457	8	ABU44934	Abu44934	Protein e
879	34	45.3	459	2	AAW11555	Aaw11555	Bacterial
880	34	45.3	460	4	AAU34883	Aau34883	E. coli c
881	34	45.3	460	4	AAU38115	Aau38115	Salmonell
882	34	45.3	460	6	ABU48402	Abu48402	Protein e
883	34	45.3	460	6	ABU28887	Abu28887	Protein e
884	34	45.3	461	4	ABU46963	Abu46963	Protein e
885	34	45.3	462	8	AAM39523	Aam39523	Human pol
886	34	45.3	462	8	ADN25462	Adn25462	Bacterial
887	34	45.3	466	2	AAW72230	Aaw72230	HSV-2 str
888	34	45.3	476	8	AAR71323	Aar71323	Acetyl-Co
889	34	45.3	476	8	ADJ49745	Adj49745	Oil-assoc
890	34	45.3	476	8	ADP83249	Adp83249	Full leng
891	34	45.3	479	8	AAU39195	Aau39195	Propionib
892	34	45.3	479	5	ADR41457	Adr41457	Human CD-
893	34	45.3	479	4	ABM35714	Abm35714	Propionib
894	34	45.3	481	8	AAU02920	Aau02920	Angiotens
895	34	45.3	483	8	ABM47716	Abm47716	Human dia
896	34	45.3	485	4	AAM41154	Aam41154	Human pol
897	34	45.3	500	2	AAR12771	Aar12771	C1 inhibi
898	34	45.3	500	2	AAR12772	Aar12772	C1 inhibi
899	34	45.3	500	2	AAR12771	Aar12771	C1 inhibi
900	34	45.3	500	2	AAR12773	Aar12773	C1 inhibi

ID			Len	N	Accession	Accession	Description
901	34	45.3	500	2	AAR12770	Aar12770	C1 inhibi
902	34	45.3	500	2	AAR12117	Aar12117	C1 inhibi
903	34	45.3	500	2	AAR12769	Aar12769	C1 inhibi
904	34	45.3	500	2	AAW18213	Aaw18213	Recombina
905	34	45.3	500	2	AAW18215	Aaw18215	Recombina
906	34	45.3	500	2	AAW18212	Aaw18212	Recombina
907	34	45.3	500	2	AAW18212	Aaw18212	Recombina
908	34	45.3	500	2	AAW18207	Aaw18207	Wild-type
909	34	45.3	500	2	ADE83541	Ade83541	Human Pro
910	34	45.3	500	2	AAW18216	Aaw18216	Recombina
911	34	45.3	500	2	AAW18214	Aaw18214	Recombina
912	34	45.3	500	5	ADQ91254	Adq91254	Human C1-
913	34	45.3	500	5	ABG76992	Abg76992	Human C1
914	34	45.3	500	5	ABG76995	Abg76995	Human C1
915	34	45.3	500	5	ABG76994	Abg76994	Human C1
916	34	45.3	500	5	ABG76991	Abg76991	Human C1
917	34	45.3	500	5	ABG76994	Abg76994	Human C1
918	34	45.3	500	7	ADD18724	Add18724	Human dia
919	34	45.3	500	6	ADE58764	Ade58764	Novel pro
920	34	45.3	500	7	ADE08961	Ade08961	Human TRI
921	34	45.3	500	5	ADJ27205	Adj27205	M. xanthu
922	34	45.3	500	5	AEA23540	Aea23540	Bacterial
923	34	45.3	500	2	ADS43281	Ads43281	Human PRO
924	34	45.3	501	7	ABM94194	Abm94194	Human ova
925	34	45.3	502	9	ADE07878	Ade07878	HSV-2 str
926	34	45.3	513	5	ABS34464	Abs34464	Novel pro
927	34	45.3	517	7	AAB53464	Aab53464	Drosophil
928	34	45.3	518	7	ABG10021	Abg10021	Snail tra
929	34	45.3	519	4	AAY57930	Aay57930	Human col
930	34	45.3	522	8	ABP41513	Abp41513	Novel hum
931	34	45.3	523	2	ADW23857	Adw23857	Novel pro
932	34	45.3	534	7	ABB60673	Abb60673	Human EST
933	34	45.3	539	4	ABB58287	Abb58287	Human dia
934	34	45.3	539	9	ABB42811	Abb42811	Human dia
935	34	45.3	540	3	ABS34464	Abs34464	Human dia
936	34	45.3	544	3	ABG10021	Abg10021	Human dia
937	34	45.3	546	4	ABM84720	Abm84720	Human dia
938	34	45.3	546	8	ADM87619	Adm87619	Rice abio
939	34	45.3	547	8	ABM84720	Abm84720	Drosophil
940	34	45.3	547	8	ABM84721	Abm84721	Protein e
941	34	45.3	547	8	ABM84717	Abm84717	Herbicida
942	34	45.3	547	8	ABM84719	Abm84719	Bacterial
943	34	45.3	547	8	ABU19840	Abu19840	Human hCA
944	34	45.3	553	8	ABB60673	Abb60673	Influenza
945	34	45.3	575	7	ABM89158	Abm89158	Influenza
946	34	45.3	582	4	AGG91652	Agg91652	Influenza
947	34	45.3	589	8	AAW01672	Aaw01672	Influenza
948	34	45.3	589	2	AAW75444	Aaw75444	C glutami
949	34	45.3	590	4	AAE04954	Aae04954	Rice abio
950	34	45.3	590	9	AEB70991	Aeb70991	Segment o
951	34	45.3	602	9	ABB92316	Abb92316	HSV-2 str
952	34	45.3	608	9	ABB73230	Abb73230	Segment o
953	34	45.3	608	9	AEB73304	Aeb73304	Bacterial
954	34	45.3	610	2	AAW72228	Aaw72228	Angiotens
955	34	45.3	619	2	ADC12742	Adc12742	Bacterial
956	34	45.3	620	8	ADN23006	Adn23006	Salmonell
957	34	45.3	636	4	AAU02972	Aau02972	E. coli c
958	34	45.3	649	2	AAW72097	Aaw72097	HSV-2 str
959	34	45.3	678	7	ABU35712	Abu35712	Mouse fri
960	34	45.3	685	2	AAW31274	Aaw31274	Mouse fri
961	34	45.3	685	8	AAW31274	Aaw31274	Protein e
962	34	45.3	685	9	ADG74272	Adg74272	Mouse fri
963	34	45.3	685	8	AAU74823	Aau74823	Mouse GPC
964	34	45.3	685	9	ADX16341	Adx16341	Mouse fri
965	34	45.3	685	8	ADO29340	Ado29340	Mouse GPC
966	34	45.3	694	6	ADP75320	Adp75320	Human REP
967	34	45.3	694	6	AAE34057	Aae34057	Human pro
968	34	45.3	694	7	ABU55903	Abu55903	Human pro
969	34	45.3	694	7	ADG74271	Adg74271	F2D 8 pro
970	34	45.3	694	8	ADN40026	Adn40026	Prostate
971	34	45.3	694	8	ADG74271	Adg74271	Human fri
972	34	45.3	694	8	ADO22266	Ado22266	Cancer/an
973	34	45.3	694	8	ADR46693	Adr46693	Human fri

RESULT 1

ID   ADM75918 standard; peptide; 15 AA.
XX
AC   ADM75918;
XX
DT   03-JUN-2004   (first entry)
XX
DE   Human MHC class II binding human Factor VIII peptide G.
XX
KW   human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
KW   MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
XX
OS   Homo sapiens.
XX
XX
PN   WO2003087161-A1.
XX
PR   23-OCT-2003.
XX
PF   17-APR-2003; 2003WO-EP004063.
XX
PR   18-APR-2002; 2002EP-00008712.
PR   24-MAR-2003; 2003EP-00006554.
XX
PA   (MERE) MERCK PATENT GMBH.
XX
PI   Jones T, Baker M, Carr FJ;
XX
DR   WPI; 2003-845307/78.
XX
PT   New modified human Factor VIII molecule being substantially non-
PT   immunogenic or less immunogenic than non-modified human Factor VIII,
PT   useful in preparing a composition for treating e.g., Gaucher's disease.
XX
PS   Disclosure; Page 10; 68pp; English.
XX
CC   The invention relates to a novel modified human Factor VIII molecule. The
CC   modified human Factor VIII molecule being substantially non-immunogenic
CC   less immunogenic than a non-modified human Factor VIII and having
CC   essentially the same biological specificity and activity when used in
CC   vivo. The modified human Factor VIII molecule comprises specifically

ALIGNMENTS

974	34	45.3	694	9	Adx16339	Human fri
975	34	45.3	694	9	Aeb28132	Human fri
976	34	45.3	715	2	Adb65231	Human pro
977	34	45.3	715	2	Aaw61533	Human Fas
978	34	45.3	740	4	Aab69149	Human dax
979	34	45.3	740	4	Aau00631	Human dea
980	34	45.3	740	7	Adb82732	Human pro
981	34	45.3	740	7	Adj69474	Human hea
982	34	45.3	740	8	Abm80752	Tumour-as
983	34	45.3	740	8	Adx05576	Cyclin-de
984	34	45.3	741	7	Adm27072	Hyperther
985	34	45.3	751	4	Aag92771	C_glutami
986	34	45.3	757	5	Abf66129	Bifidobac
987	34	45.3	777	7	Adm04504	Human pro
988	34	45.3	784	5	Abb93947	Herbicida
989	34	45.3	784	8	Adn73567	Thale cre
990	34	45.3	822	7	Add13667	C. glutam
991	34	45.3	890	4	Abg08340	Novel hum
992	34	45.3	905	8	Adq08724	Ciona int
993	34	45.3	906	9	Aeb53801	Drosophil
994	34	45.3	934	9	Ady60907	Abiotic s
995	34	45.3	940	8	Adf42722	Mouse MPI
996	34	45.3	1025	7	Adf06827	Bacterial
997	34	45.3	1072	7	Adc83636	LTRPC3-re
998	34	45.3	1072	8	Adc93477	Murine tr
999	34	45.3	1106	8	Adl82993	Human PRO
1000	34	45.3	1106	9	Ady14329	PRO polyp

CC   altered amino acid residues compared with the non-modified parental
CC   molecule, where the altered amino acid residues cause a reduction or an
CC   elimination of one or more of the T-cell epitopes, which act in the
CC   parental non-modified molecule as MHC class II binding ligands and
CC   stimulate T-cells. The potential MHC class II binding peptide is
CC   useful for the manufacture of the modified Factor VIII molecule or a
CC   vaccine in order to reduce immunogenicity to Factor VIII in a patient.
CC   The modified Factor VIII molecule is useful in preparing a composition
CC   for treating e.g., Gaucher's disease. This sequence represents a human
CC   Factor VIII peptide with potential human MHC class II binding activity of
CC   the invention.
XX
SQ   Sequence 15 AA;

Query Match   100.0%; Score 75; DB 7; Length 15;
Best Local Similarity   100.0%; Pred. No. 1.7e-06;
Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MSSSPHVLRNRAQSG 15
               |||||||||||||||
Db   1 MSSSPHVLRNRAQSG 15

RESULT 2

ADM75967

ID   ADM75967 standard; peptide; 15 AA.
XX
AC   ADM75967;
XX
DT   03-JUN-2004   (first entry)
XX
DE   Human MHC class II binding human Factor VIII proliferative peptide #45.
XX
KW   human Factor VIII; non-immunogenic; immunogenic; T-cell epitope;
KW   MHC class II; ligand; vaccine; immunogenicity; Gaucher's disease.
XX
OS   Homo sapiens.
XX
PN   WO2003087161-A1.
XX
PD   23-OCT-2003.
XX
PF   17-APR-2003; 2003WO-EP004063.
XX
PR   18-APR-2002; 2002EP-00008712.
PR   24-MAR-2003; 2003EP-00006554.
XX
PA   (MERE) MERCK PATENT GMBH.
XX
PI   Jones T, Baker M, Carr FJ;
XX
DR   WPI; 2003-845307/78.
XX
PT   New modified human Factor VIII molecule being substantially non-
PT   immunogenic or less immunogenic than non-modified human Factor VIII,
PT   useful in preparing a composition for treating e.g., Gaucher's disease.
XX
PS   Disclosure; Page 20; 68pp; English.
XX
CC   The invention relates to a novel modified human Factor VIII molecule. The
CC   modified human Factor VIII molecule being substantially non-immunogenic
CC   or less immunogenic than a non-modified human Factor VIII and having
CC   essentially the same biological specificity and activity when used in
CC   vivo. The modified human Factor VIII molecule comprises specifically
CC   altered amino acid residues compared with the non-modified parental
CC   molecule, where the altered amino acid residues cause a reduction or an
CC   elimination of one or more of the T-cell epitopes, which act in the
CC   parental non-modified molecule as MHC class II binding ligands and
CC   stimulate T-cells. The potential MHC class II binding peptide is
CC   useful for the manufacture of the modified Factor VIII molecule or a
CC   vaccine in order to reduce immunogenicity to Factor VIII in a patient.
CC   The modified Factor VIII molecule is useful in preparing a composition
CC   for treating e.g., Gaucher's disease. This sequence represents a human